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/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-449-609-10 + 435.50 824.45 3.1e-38 /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-487-368A-3 + 434.50 817.67 7.4e-38 /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-487-368A-10 + 433.50 812.31 1.5e-37 /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-811-481-30 + 432.00 826.47 2.4e-38 /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-811-481-30 + 432.00 824.30 3.2e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 ATGGACCAAAGAGAAATTCTGCAGAAGTTCCTGGATGAGGCCCAAAGCAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 sLysIleThrLysGluGluPheAlaAsnGluPheLeuLysLeuLysArgG 34
                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-081-345-1
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Percent Identity: 99.416
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                                                                                                                                                                                                                                APPLICANT: Bahija Jallal
APPLICANT: Gregory D. Plowman
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: PTP04 RELATED DISORDERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: IBM P.C. DOS 5.C SOFTWARE: FASTSED for Windows 2.0 CURRENT APPLICATION DATA: 05/09/081,345 FILLING DATE: HETEWITh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J. RECISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 334/253
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: MAY 20, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                          Sequence 1, Application US/09081345
Patent No. 6228641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-600-358A-4 x US-09-081-345-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3580 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 3543.50
Ratio: 5.188
nilarity: 99.708
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                            _documentation_block:
                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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824.30
818.86
818.86
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                                                                            About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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Database length: 122816752
Search time (sec): 76.930000
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                                      Date: May 26, 2002 1:06 PM
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from: 1

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Page

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Align seg 1/1 to: US-08-951-260A-1
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    Patent No. 6004791
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    APPLICANT: Nachito
    APPLICANT: Ulrich, Axel
    TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
    TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
    NUMBER OF SQUENCES: 7
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-951-260A-1
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PURIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,860
FILING DATE: No. 6004791ember 13, 1996
APPLICATION NUMBER: PCT/1897/00946
FILING DATE: June 17, 1997
ATTORNEY/ABORT INFONMATION:
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REERRENEE/ADCKET NUMBER: 227/004
TELECOMMUNICATION INFORMATION:
TELECHONE: (213),489-1600
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,260A
FILING DATE: October 16, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2226 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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3.041
68.908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                         2100 AATCA 2104
                                                                                                                                                                                                                 684 ysSer 685
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    Patent No. 6238902
    GENERAL INCEMATION:
    APPLICANT: Cheng, Jill
    APPLICANT: Lausky, Laurence A.
    TILE OF INVENTION:
    FILE REFERENCE: P1010R1
    CURRENT FILIG DATE: 1997-03-20
    NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 6
Percent Identity: 44.037
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3.069
73.394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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    SERERAL INFORMATION:
    APPLICANT: Tonks, Nicholas K. and stman, Arne
    TITLE OF INFORMION: Density Enhanced Protein Tyrosine Phosphatase;
    NUMBER OF SEQUENCES: 6
    CORRESPONDENCE ADDRESS:
                                                                                                                                                384 TGGGGTCAAGGTAATCCTGATGGCCTGTCAAGAGACAGAAATGGACGGA 433
                                                                                                                                                                                                                                                                    203 AspProlleLeuGluLeuIleTrpAspValArgCysTyrGlnGluAspAs 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 nArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValTyrAsnA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 laValLeuGluLeuPheLysArgGlnMetAspValIleArgAspLysHis 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 SerGlyThrGluSerGlnAlaLySHisCysIlePro.....GluLysAs 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           919 CCCCAATACCAGAACCTCAAGGAGAACTGCGCTCCAATCTGCAAGGAAGC 968
169 rIleIleArgThrLeuLysValLysPheAsnSerGluThrArgThrIleT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, Suite 6300 CITY: Chicago STATE: 11linois STATE: 11linois 21P: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 GlyProPheSerValSerCysGluAlaGluLysArg...LysSerAspTy
                                                                                                                                                                                                                                                                                                                                                    186 yrGlnPheHisTyrLysAsnTrpProAspHisAspValProSerSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                      236 alileCysAlaIleValAspTyrThrTrpMetLeuLeuLysAspGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 rSerValLeuIleIleValMetAlaCysMetGluTyrGluMetGlyLysL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 IleProGluAsnPheSerValPheSerLeuIleArgGluMetArgThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seg_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-854-585-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 nHisThrLeuGlnAlaAspSerTyrSerPro 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               969 TITCICCCICAGGACCICCICAGCCCIGCCT 999
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MEDIUM TYPE: Floppy disk
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3448 GCAAGCTGACTCCAACTGTGGGTTCGCAGAGAATACGAAGATCTGAAGC 3497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 LeuSerThrThrLeuLeuAspPheTrpArgMetIleTrpGluTyrSerVa 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 lLeuIleIleValMetAlaCysMetGluTyrGluMetGlyLysLysLysC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ysGluArgTyrTrpAlaGluProGlyGluMetGlnLeuGluPheGlyPro 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 LysLysAsnArgTyrLysAspIleLeuProTyrAspTyrSerArgValG1 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 GlnSerLysLysIleThrLysGluGluPheAlaAsnGluPheLeuLysLe 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 .....ThrTyrProThrThrValAlaGluAsnAlaLysAsnIle 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 7
Percent Identity: 38.305
                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854.585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-854-585-1 from: 1 to: 5117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                          HILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: BOTUN, MICHAEL F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMUNICATION INFORMATION:

TELEPAN: 312-474-6300

TELEPAN: 312-474-6300

TELEPAN: 312-474-0448

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5117 base, pairs
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/237,940
FILING DATE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-600-358A-4 x US-08-854-585-1
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2.579
66.780
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STRANDEDNESS: single
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350..4364
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Ratio:
Percent Similarity:
                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-854-585-1
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3889 AGATITCACAGTGAAAATAICCAGACAAGTGAGAGTCACCCTCTGAGAC 3938
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                                                    156 PheSerValSerCysGluAlaGluLysArgLysSerAspTyrIleIleAr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 lyVallleCysAlaIleValAspTyrThrTrpMetLeuLeuLysAspGly 251
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                                                                                                   3839 ATAACTGTGGCAATGACATCAGAAATTGTTCTTCCGGAATGGACCATCAG
                                                                                                                                                    172 gThrLeuLysValLys.....PheAsnSerGluThrArgThrIleTyrG
                                                                                                                                                                                                                                                                                                                                                   204 ProlleLeuGluLeuIleTrpAspValArgCysTyr.....GlnGluAs
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GENERAL INFORMATION:
APPLICANT: TONKS, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Borun STREET: 233 South Wacker Drive, Suite 6300 CITY: Chicago STRTE: 1111nois COUNTRY: United States of America 21P: 66006
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION: TELEPHONE: 312-474-6300
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TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 5117 base pairs
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3498 TTGTTGGAATTAGTCAACCTAAATATGCAGCAGAACTGGCTGAGAATAGA 3547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 uLeuSerLeuIleThrSerAspGluAspSerSerTyrIleAsnAlaAsnP 89
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                                                                                                                                                                                                                                                                                                                                              Percent Identity: 38.305
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                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-600-358A-4 x PCT-US95-05512-1
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                        508.00
2.579
66.780
                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 350..4364
PCT-US95-05512-1
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Quality:
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1139 ACCGTG......GATGTGTATGGGATTGTGTATGACCTTCGAAT 4176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 rGlnArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValTyrA 285
                                                                                                                                  235 lyvalileCysAlaIleValAspTyrThrTrpMetLeuLeuLysAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-018-129-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Vogel, Wolfgang
TITLE OF INVENTION: PHO 1D: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Avenue of Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: LIPPPY disk
COMPUTER: IBM PC COMPATIBLE
ORPRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATOALIN PC-Base #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/018,129
FILING DATE: 19930216
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
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Percent Identity: 31.293
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1155 Avenue of Americas
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    Sequence 4, Application US/08018129
    patent No. 5589375
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MOLECULE TYPE: DNA (genomic)
FEATURE:
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1.968
57.143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-018-129-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
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US-09-600-358A-4 x US-08-018-129-4	166
14 AlaGInSerLysLysIleThrLysGluGluPheAlaAsnGluPh	299
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47 hrvalalagluasnalaLysasnileLysLysasnargTyrLysaspile 63 :::::::::::::::	181
64 LeuProTyraspTyrSerargValGluLeuSerLeuIleThrSeraspGl 80 ::: :::::	186
80 uAspSerSerTyrIleAsnAlaAsnPheIleLysGlyValTyr 94 	191
95GlyProlysalaTyrIlealaThrGlnGly 104 	1967
105 ProLeuSerThrThrLeuLeuAspPheTrpArgMetlleTrpGluTyrSe 121 	2010
121 rValLeulleIleValMetAlaCysMetGluTyrGluMetGlyLysLysL 138 : ::: ::: ::: 1176 CTCCCGAGTGATGTCATGACAACGAAGAGGAGAGGAAAGAGTA 1225	206.
138 ysCysGluargTyrTrpalaGluProGlyGluMetGlnLeuGluPhe 153	2114
154 GlyPropheserValserCysGlualaGluLysargLysSerAspTyrIl 170 ::: 1270 GGCGTCATGCGTGTTAGGAACGTCCAAGAAGAAGCGCCGCTCATGACTATAC 1319	seq_name seq_docu
170 elleargThrLeuLysValLysPheAsnSerGluThra 183 ::: ::: 1320 GCTAAGAGAACTTAAAGCTTGGAAAGGAATACGGAGA 1366	GENE
183 rgThrIleTyrGlnPheHisTyrLysAsnTrpProAspHisAspValPro 199 ::::: ::: ::::	L L L L L L L L L L L L L L L L L L L
200 SerSerlleAspProlleLeuGluLeulleTrpAspValArgCysTyrGl 216 	
216 nGluAspAspSerValProIleCys1leHisCysSeralaGlyC 231 :: :: ::	
231 ysGlyArgThrGlyVallleCysAlalleValAspTyrThrTrpMetLeu 247 	
248 LeuLysaspGlylleIleProGluasnPheSerValPheSerLeuIlear 264 	PR
264 gGlumetArgThrGlnArgProSerLeuValGlnThrGlnGluGlnTyrG 281 : ::: :: :::::	ATI
281 luLeuValTyrAsnAlaValLeuGluLeuPheLysArgGln 294	

1664 GATTATCTATATGCGGTCCAGCATTATATTGAAACACTACAGCGCAGG	:::::: :::
295 MetAsp	:
. დ	CGAATATACAAATAT 1763
297VallleArgAspLysHisSerGlyThrGluSerGlnAlaLysH ::: :::	luSerGlnAlaLysH 311 :: RGAGCCCTCTCCCGC 1813
	315
CTIGI	18
316LysAsnHisThrLeuGlnAlaAspSerTyrSerPr 	rSerPr 327 AGTTTCAGATGAGA 1913
327 oAsnLeuProLys	aA 337
1914 AAACCTGCCAAAACTTCAGCACAGAAATAGATGTGGACTTT	CC 19
337 laLysMethetasnGlnGlnargThrLysMetGluIleLysGluSerSer	IleLysGluSerSer 353 ::: ::::: STGAAGTCTGAATTT 2013
	366
2014 GGATTTGGAAGGCTTGCAATGTGGTTGACTACCTTTTGATAAGCAAAATT	ITGATAAGCAAAATT 2063
366 uGluLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuG 1	erPheAspPheLeuG 383 ::::: CAATACCTGCTTCCC 2113
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-	1
<pre>seq_documentation_block: ; Sequence 4, Application US/08448250 ; Patent No. 5981251</pre>	
INFORMATION:	
VOGEL, WOILGAING VENTION: PTP 1D: A NOVEL PROTEIN VENTION: PHOSPHATASE	OTEIN TYROSINE
R OF SEQUENCES: SPONDENCE ADDRES	
വംഗ	
; CITY: New York ; STATE: New York	
; COUNTRY: U.S.A. ; ZIP: 10036	
PUTER	
ER: IBM PC compatible ING SYSTEM: PC-DOS/MS	
PatentIn Release #1.0, Version #	
APPLICATION NUMBER: US/08/448,250	
CCATION	
LICATION NU	
G DATE: 16-FE Y/AGENT INFORM	
; NAME: Misrock, S. Leslie ; REGISTRATION NUMBER: 18,872	
- CO 24.	

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1270 GGCGTCATGCGTTAGGAACGTCAAAGAAAGCGCCGCTCATGACTATAC 1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 GlyProPheSerValSerCysGluAlaGluLysArgLysSerAspTyrIl 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 rValLeuIleIleValMetAlaCysMetGluTyrGluMetGlyLysLysL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 ysCysGluArgTyrTrpAlaGluProGlyGluMetGlnLeu...GluPhe 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 elleArgThrLeuLysVal...........LysPheAsnSerGluThrA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 rgThrIleTyrGlnPheHisTyrLysAsnTrpProAspHisAspValPro 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         926 AAGAGGGTCAAAGGCAAGAAAACAAAAACAAAATAGATATAAAAACATC 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  888 ACTACAACAACAGGAGTGCAAACTT......CTCTACAGCCGAA 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 sLeuLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThrT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 hrValAlaGluAsnAlaLysAsnIleLysLysAsnArgTyrLysAspIle 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 LeuProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAspGl 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AlaGlnSerLysLysIleThrLysGluGluPheAlaAsnGluPheLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 15
Percent Identity: 31,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 2790
                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                     TELEPHONE: (212) 790-9090
TELERA: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2790 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-600-358A-4 x US-08-448-250-4
                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 496.00
Ratio: 1.968
nilarity: 57.143
                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 130..1911
US-08-448-250-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                          TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
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                                                                                                                                                                                                                                                     FEATURE
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1864 GTCTATGAAAACGTGGGCCTGATGCAACAGCAGAAAGTTTCAGATGAGA 1913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1814 CITGIACTCCTTCGCCACCCTGTGCAGAAATGAGAGAGACAGTGCTAGA 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 SerPheAsp.....PheArgThrSerGluIleSerAlaLysGl 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 uGluLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 luLeuValTyrAsnAlaVal.....LeuGluLeuPheLysArgGln 294
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                                                                                                                                                                                                                                                                                                                         LeuLysAspGlyIleIleProGluAsnPheSerValPheSerLeuIleAr 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 ......ValIleArgAspLysHisSerGlyThrGluSerGlnAlaLysH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 isCysIleProGlu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1914 AAACCTGCCAAAACTTCAGCACAGAAATAGATGTGGACTTTCACCTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 laLysMetMetAsnGlnGlnArgThrLysMetGluIleLysGluSerSer
                                                                                                                                         nGluAsp.....AspSerValProIleCysIleHisCysSerAlaGlyC
                                             SerSerIleAspProlleLeuGluLeuIleTrpAspValArgCysTyrGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....LysAsnHisThrLeuGlnAlaAspSerTyrSer.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 luLeuAsnTyrSerPheAspLys 390
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Fuchs, Miriam
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APPLICANT:
APPLICANT:
APPLICANT:
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                                             200
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319	CysilePro	31.
35		350
311	0 AspLysHisSerGlyThrGluSerGlnAlaLysHis	. 30
3507		345
299	1PheLysArgClnMetAspValileArg	29.
4	- 15 15	0
. 6	יייס זיין באים ונפאפן עם	
285	9 GlnArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValTyrAs	26
3357	<pre>2 lelleProGluAsnPheSerValPheSerLeuIleArgGluMetArgThr</pre>	332
3319	AspTyr' ATCATG	327
3269	:::::	322
m	Val ProlleCys1leHisCysSerAlaGlyCysGlyArgThrG	21
218 3219	<pre>2 LeAspProlleLeuGluLeulle</pre>	317
\vdash	0 TAAACAGTICCATTTCACGGGCTGGCCTGACCATGGAGTGCCCTAC	312
202	InPheHisTyrLysAsnTrpProAspHisAa	18
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185	ArgThrLeuLysValLysPhcAsnSerGluThrArgThrI	17
3069	4 lyPropheSerValSerCysGluAlaGluLysArgLysSerA ::: ::: 0 GTGACTTCAAAGTAAGGTGTGTAGAAATGGAACCACTTGCTG	302
3019	7 sLysCysGluargTyrTrpalaGluProGly ::: 9 TAAATGCTATAAATATTGGCCTGATGATACT	13
2978	S	292
6		
120	4 lyProLeuSerThrThrLeuLeuAspPheTrpArgMetlleTrp	10

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3819 AAACGAAGTCGACTTGTCCCAGGGCTGCCCTCAGTACTGGCCAGAGAAG 3868
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                                                                                                                                                                                                                                   402 laPhe.....ProlleValGlyGluProLeuGlnLySHisGln 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ullrich, Axel
APPLICANT: Vogel, Wolfgang
APPLICANT: Puchs, Milam
IITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
IITLE OF INVENTION: PHOSPHATASE-KAPPA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-087-244A-4
                                                                                             3769 GACTICIGGAGAITAGIGIAIGAITAIGGCIGIACCICCAIIGIGAIGIT
                                                                                                                                        ......AspLysAsnAlaAspThrThrMetLysTrpGlnThrLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/087,244A
FILING DATE: 01-UUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7683-042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION UNDBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-
TELECOMMUNICATION INFORMATION:
TELEFRAN: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
APPLICANT: Ullrich, Axel
                                               380 AspPheLeuGluLeuAsnTyrSerPhe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 4651 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
1..4317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5863755
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-087-244A-4
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3019
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                                                                                                                                                                                                                               2703 TTGG.....GATGTAGCTAAAAAGATCAAA 2728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 lyProPheSerValSerCysGluAlaGluLysArgLysSerAspTyrIle 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 yValileCysAlaileValAspTyrThrTrpMetLeuLeuLysAspGlyI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 lelleProGluAsnPheSerValPheSerLeulleArgGluMetArgThr 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerValLeuIleIleValMetAlaCysMetGluTyrGluMetGlyLysLy 137
                                                                                                                                                                                                                                                                                                                                                                    54 snileLysLysAsnArgTyrLysAspIleLeuProTyrAspTyrSerArg 70
                                                                                                                                                                                                                                                                                     37 sTyrLysAlaAspLysThrTyrProThrThrValAlaGluAsnAlaLysA 54
                                                                                                                                                                                                       21 LysGluGluPheAlaAsnGluPheLeuLysLeuLysArgGlnSerThrLy 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3220 AGTGCTGGCCCCATCGTTGTACATTGCAGTGCTGGTGCTGGACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::|||::::||| | | | | :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aAsnPheIleLysGlyValTyrGlyProLysAlaTyrIleAlaThrGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2929 CAATCTGCTTGCATTGTGATGGTTACAAATTTAGTTGAGGTTGGCCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 sLysCysGluArgTyrTrpAlaGluProGlyGluMetGlnLeuGluPheG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 eTyrGlnPheHisTyrLysAsnTrpProAspHisAspValProSerSerI : |||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3270 CTGCTACATTGTGATTGACATCATGCTAGACATGGCTGAAAGAGAGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 AspSerValProIleCysIleHisCysSerAlaGlyCysGlyArgThrGl
               Length: 467
Gaps: 16
Percent Identity: 29.122
                                                                                                                                                               from: 1
                                                                                                                                                               Align seg 1/1 to: US-08-087-244A-4
                                                                                                  alignment_block:
US-09-600-358A-4 x US-08-087-244A-4
               492.50
1.954
53.961
                 Quality:
Ratio:
Percent Similarity:
alignment_scores
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	285 3408 291 3458	National National	290 3457 299 3507
	348 3705 363 3733 380 3769 389 3819	Gacadcaccaccaccaccaccaccaccaccaccaccaccac	363 3732 379 3768 3818 402 3868
GGACGAGCTACAGGGGAACCAGGTGCTTTC eralaLysGluGluLeuValLeuHisProAlaLysSerSerThrSerPhe ::: ::: ::: AspPheLeuGluLeuValTeCATACCCTCTGCCAAACAAAA AspPheLeuGluLeuAsTTyrSerPhe :::	402 3869 (415 3919 (431 (431 (431 (431 (431 (431 (431 (431	iapheProllevalGlyGluProLeuGlnLysHisGln :::: :GaTGCTACGATATGGCCCATCCAAGTGAATGTATGTCTTGTTCATG :::: :GaTGCTACGATATGGCCCATCCAAGTGAATGTATGTCTTGTTCATG ::::::::::::::::::::::::::::::::::::	414 3918 431 3968
GGACAGCTACAGGTACTTC GIUIleLysGluGerSerSerPheAspPheArgThrSerGluIleS GGACAGCTACAGGTACTGTTTC eralaLysGluGluLeuValLeuHisProAlaLysSerSerThrSerPhe ::: ::: ::: ::: ::: ::: :::	document equence = atent No. GENERAL I APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA CORREST CORREST CORREST COUNT STREE STREE STREE COUNT	documentation_block: quence 5, Application US/08202389 tent No. 536536 ENERAL INFORMATION: APPLICANT: Freeman Jr., Robert M. APPLICANT: Plutzky, Jorge APPLICANT: Rosenberg, Robert D. APPLICANT: Lexington Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: MA.	

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1035 CGGGTCCGACTACATGCCAACTACATCAAGAACCAGCTGCTAGGCC 1084
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847 GAGTCCGAGGATACAGCCAGGCTGCTTCTGGGAGGAGTTTGAGAGTT 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              897 GCAGAAGCAGGAGGTGAAG......AACTTGCACCAGCGTCTGG 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 GlnSerLysLysIleThrLysGluGluPheAlaAsnGluPheLeuLysLe 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 uLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThrThrV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 uAspSerSerTyrIleAsnAlaAsnPheIleLysGly...ValTyrGlyP 96
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,389
FILING DATE: 28 FEB-1994
FILING DATE: 01-DEC-1992
PRIOR APPLICATION UDBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION NUMBER: US 07/829,141
FILING DATE: 31-JAN-1992
PRIOR APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-JUN-1991
ATDORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-JUN-1991
ATDORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: B1H92-05MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEO ION: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2145 base pairs
TYPE: UNDELS: double
TTREE OUGLE CACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 14
Percent Identity: 32.990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-202-389-5 from: 1 to: 2145
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Ratio: 2.021
Percent Similarity: 62.113
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; LOCATION: 145..1929
US-08-202-389-5
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1749 GTACGGGAACATC.....ACCT 1765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1816 AAACACAAGGAGGATGTGTATGAGAACCTGCACACTAAGAACAAGAGGGA 1865
                                                                                              338
                                 1135 ACAGTCAATGACTTCTGGCAGATGGCGTGGCAGGAGAACAGCCGTGTCAT 1184
                                                                                                                                                     158
                                                                                                                                                                                                                              SerCysGluAlaGluLysArgLysSerAspTyrIleIleArgThrLeuLy 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1432 CTCAGCTTCCTGGACCAGATCAACCAGGGGGGGGAAAGTCTGCCTCACGC 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ......GACATGCIC 1551
ThrLeuLeuAspPheTrpArgMetIleTrpGluTyrSerValLeuIleIl 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 rValProlleCyslleHisCysSerAlaGlyCysGlyArgThrGlyValI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 sMetGluIleLysGluSerSerSerPheAspPheArgThrSerGluIleS 363
                                                                                                                                                                           1332 GETCTCCCCGCTGGACATGGAGACCTGATTCGGGAGATCTGGCATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 leCysAlaIleValAspTyrThrTrpMetLeuLeuLysAspGlyIleIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 yrSerProAsnLeuProLysSerThrThrLysAlaAlaLys.....
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                                                                                                                                                                                                                                                                                                       sValLys.....PheAsnSerGlu...ThrArgThrIleTyrGlnPheH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 ....IleArgGluMetArgThrGlnArgProSerLeuValGlnThrGlnG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nAlaLysHisCysIleProGluLysAsnHisThrLeuGlnAlaAspSerT
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                                                                                                                                                   142 yrTrpAlaGluProGlyGluMetGlnLeuGluPheGlyProPheSerVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1916 CCCTCAAGAGGAAG 1929
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109
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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-358-685-1

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1301
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APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-1 EXPRESSION
FILE REFERENCE: TS-0081
CURRENT APPLICATION NUMBER: US/09/358,685
CURRENT APPLICATION NUMBER: 1999-07-21
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 SerCysGluAlaGluLysArgLysSerAspTyrIleIleArgThrLeuLy 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 ThrLeuLeuAspPheTrpArgMetIleTrpGluTyrSerValLeuIleIl 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 sValLys.....PheAsnSerGlu...ThrArgThrIleTyrGlnPheH 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 uLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThrThrV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eValMetAlaCysMetGluTyrGluMetGlyLysLysLysCysGluArgT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 GlnSerLysLysIleThrLysGluGluPheAlaAsnGluPheLeuLysLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 alAlaGluAsnAlaLysAsnIleLysLysAsnArgTyrLysAspIleLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 yrTrpAlaGluProGlyGluMetGlnLeuGluPheGlyProPheSerVal
                                                                                                                                                                                                                                                                                                                                                                        Length: 388
Gaps: 14
Percent Identity: 32.990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1 to: 2277
            Sequence 1, Application US/09358685 Patent No. 6121047
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US-09-600-358A-4 x US-09-358-685-1
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2.012
62.113
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US-09-358-685-1
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
seq_documentation_block:
                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            Ouality:
                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                     LENGTH: 2277
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1649 TCATTGTCATC.....GACATGCTC 1668
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Sequence 7, Application US/08202389
Patent No. 5536636
GENERAL INFORMATION:
APPLICANT: Freeman Jr., Robert M.
APPLICANT: Plutzky, Jorge
APPLICANT: Neel, Benjamin G.
APPLICANT: Nosenberg, Robert D.
TITLE OF INVENTION: IDENTFICATION OF NOVEL TYROSINE
TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                    206 LeuGluLeuIleTrpAspValArgCysTyrGlnGluAsp.....AspSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2033 CCCTCAAGAGGAAG 2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 erAlaLysGluGlu 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Lexington STATE: MA
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96 ro.......LysalaTyrIleAlaThrGlnGlyProLeuSerThr 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 ProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAsp...Gl 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 alAlaGluAsnAlaLysAsnIleLysLysAsnArgTyrLysAspIleLeu 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 uAspSerSerTyrIleAsnAlaAsnPheIleLysGly...ValTyrGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 GlnSerLysLysIleThrLysGluGluPheAlaAsnGluPheLeuLysLe
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Percent Identity: 31.603
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
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APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-UNN-1991
ATTONNEY, AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKT NUMBER: 32,227
REFERENCE/DOCKT NUMBER: BIH92-05MA
TELECHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2143 base pairs
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US-09-600-358A-4 x US-08-202-389-7
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59.142
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STRANDEDNESS: double
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
COCATION:
US-08-202-389-7
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392 AlaAspThrThrMetLysTrpGlnThrLysAlaPheProIleValGlyGl 408
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    Sequence 11 Application US/08202389
    Patent No. 5536636
    GENERAL INFORMATION:
    APPLICANT: Freeman Jr., Robert M.
    APPLICANT: Preeman Jr., Robert M.
    APPLICANT: Rosenberg, Robert D.
    APPLICANT: Rosenberg, Robert D.
    TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
    NUMBER OF SEQUENCES: 54
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
    STREET: Two Militia Drive
    CITY: Lexington
                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-202-389-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,389
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141
FILING DATE: 13-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141
FILING DATE: 26-JUN-1991
ATTORNEY/AGENT INPORMATION:
NUMBE: GTANDATE: PATICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Gaps:
                                                                                                                                                                                                                                                 1952 CATGCCTCAGCCCTGACCCTGTGGAAGCA 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIH92-05MA
                                                                                                                                                                                                  425 lyCysSerAsnSerLysProValAsnAla 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2276 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483.00
1.851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114..1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Lexi
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-202-389-11
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1586	CAAAACCATCCAGATGGTGCGGTCTCAGAGGTCAGGGATGGTCCAGACAG 1635	35
277	inGluGlnTyrGluLeuValTyrAsnAlaValLeuGluLeu 290	0
1636	:	85
291	PheLysArgGlnMetAsp296	9
1686	CTACAGCGCAGGATTGAAGAAGAGCAGAAAAGCAAGAGGAAAAGGGCACGA 173	35
297	vallleArgAspLysHisSerGlyThrGluS 307	7
1736	ATATACAAATATTAAGTATTCTCTAGCGGACCAGACGAGTGGAGATCAGA 178	82
307	erGlnAlaLysHisCysIleProGluLysAsnHisThrLeuGlnAlaAsp 323	m
1786	GCCCTCTCCCGCCTTGTACTCCA	80
324	SerTyrSerProAsnLeuProLysSerThrThrLysAlaAlaLysMetMe 340	0 ;
1809	ACGCCACCTGTGCAGAATGAG 183	. d
340 1832	TASDGIDGIDALGIDALDYSMEUGIUIIELYSGIDSETS 353 T.:.::::::::::::::::::::::::::::::::::	3
353	erSerPhe.AspPheArgThrSerGluIleSerAlaLysGluGluLe 368	ω
1882	193	31
9 (uValLeuHisProAlaLysSerSerThrSerPheAspP 381	
m	198	# 8
381	heLeuGluLeuAsnTyrSerPheAspLysAsnalaAspThrThrMetLys 397	7
1982	201	19
398	TrpGlnThr	69
410	uGlnLysHisGlnSerLeuAspLeuGlySerLeuLeuPheGluGlyCysS 427	7
2070	G 207	70
427	erAsnSerLysProValAsnAlaAlaGlyArgTyrPheAsnSerLysVal 443	
2071		88
444	ProlleThrArg 447	
0 6	. /ran2 6/ptod	
1 6	nentation block.	
Seguen Patent	mentarion_cros. Salabeta	
GENER	AL INFOR	
APP	Sap, Jan M.	
	APPLICANT: Ullrich, Axel APPLICANT: Vogel, Wolfgang	
	Fuchs, Miriam	
	OF INVENTION: P	
, NUM	H	
	ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas	

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2915 ACTACATTGCAACTCAAGGCCCAGTTCATGAAACCGTATATGTATTTTGG 2964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2698 AAAGAGGAATACGAGAGCTTCTTT.....GAAGGCCAGTCAGCCTC 2738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||:::|||
2865 CAACTACATCGACATTGGCTGTACAGGGATGGCTACCAGAGACCAAGCC 2914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 laTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAspPheTrp 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 ArgMetIleTrpGluTyrSerValLeuIleIleValMetAlaCysMetGl 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 aAsnPheIle......LysGlyValTyrGlyProLysA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LysGluGluPheAlaAsnGluPheLeuLysLeuLysArgGlnSerThrLy 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 sTyrLysAlaAspLysThrTyrProThrThrValAlaGluAsnAlaLysA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 ValGluLeuSerLeuIleThrSerAspGluAspSerSerTyrIleAsnAl 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 28.541
                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 24-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-449-644-3 from: 1 to: 4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                    NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-042
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH 4374 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,244
FILING DATE: 01-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-600-358A-4 x US-08-449-644-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
Quality: 478.50
Ratio: 1.899
...'arity: 53.277
                   ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..4371
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 1..4
US-08-449-644-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
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131	uTyrGluMetGlyLysLysCysGluArgTyrTrpAlaGluProGlyG ::: :: AgrGGAAGTTGGCCGGGTGAAATCCTATAAATATTGGCCTGATACTG	148 3064
148 3065	<pre>ceuGlupheGlyProPheServalSerCysGluA ::: ::: ::: </pre>	164 3105
165 3106	SeraspTyrileileargThrLeuLysVal ::::: ::: GCTGAGTATGTCGTTAGGACATTCACCTTGGAAAGG	179 3155
179 3156	rlleTyrGlnPheHisTyrI ::: :: AGTCAAACAGTTCCACTTC	196 3205
196 3206	leAspProIleLeu ::: CAACAGGGCTCCTG	212 3255
213 3256	3 F	229 3305
3306		246 3355
246 3356	uLysAspGlyIleIleProGluAs :::::: :::: AAGAGAGGGTGTGGTT	262 3393
263 3394	stargThrGlnArgProSerLeuValGlnT. :: ::::: :RGGATCTCGGCGCATTAATATGGTACAGA	279 3443
279	luLeuValTyrAsnAla ::::::::! TTTTTATTCATGATGCC	290 3493
291 3494		299 3543
300	AspLysHisSerGlyThrGlu 	310 3593
310 3594	SHISGATCCCTCGACTACAAGCTGAAGAC	313 3643
313	luLysasnHisThrLeuGlnAlaaspSe ::: aGGAACCATGACAAGAACGTTTCATGGATAT	327 3690
328	ASDLeuProLysSerThrThrLysAlaAlaLysMe	342 3740
342	nGlnArgThrLysMetGlu	357 3786
357 3787	luIleSeralaLysGluGluLeuValLeuHisFroAl: ::: ::ATGTCACACATACCC	373 3804
374	LysSerSerThrSerPheAspPheLeuGluLeu 	80 00
389	AspLysAsnAlaAspThrThrM	396

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3855 TACCTCCATCGTGATGCTAAATGAAGTGGACCTGTCTCAGGGCTGCCCAC 3904
                                                                                                                                                                                      3955 TGTATGTTCATCAATGGACTGTGATGTGATCAATCGAATTTTTAGAAT 4004
                                                                                                  3905 AGTACTGGCCAGAAGAAGGAATGCTGCGATATGGTCCTATCCAAGTGGAA 3954
                                                                                                                                                      409 ProLeuGlnLysHisGlnSerLeuAspLeuGlySerLeuLeuPheGluGl 425
                                                   ......ProlleValGlyGlu 408
                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
Sequence 3, Application US/08087244A
Sequence 3, Application US/08087244A
Patent No. 5863755
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
APPLICANT: Vogel, Wolfgang
APPLICANT: Fuchs, Mitan
TITLE OF INVENTION: PHOSPHOTYRE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-KAPPA
                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-087-244A-3
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Percent Identity: 28.541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-1993
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTIZZI, LBULTA A.
REGISTRATION NUMBER: 30,742
REFERNCE/DOCKET NUMBER: 7683-042
REFERNCE/DOCKET NUMBER: 7683-042
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPKX: 212-869-8864/9741
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 64141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-600-358A-4 x US-08-087-244A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                 396 etLysTrpGlnThrLysAlaPhe.
                                                                                                                                                                                                                                                                                           4005 ATGCAACCTAACGAGACCA 4023
                                                                                                                                                                                                                                                           425 yCysSerAsnSerLysPro 431
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1.899
53.277
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4371
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Ne COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-087-244A-3
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3065 AGGTT.....TATGGTGACTTCAAAGTCACCTGCGTAGAAATGGAG 3105
                                                                                                              ......GAAGGCCAGTCAGCCTC 2738
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                                                                                                                                                                                                                                                                                                                           ||||||||:::||||:::
2965 AGGATGGTGTGGCAAGAGCAGTCTGCCTGTATTGTGATGGTCACTAATTT 3014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3015 AGTGGAAGTTGGCCGGGTGAAATGCTATAAATATTGGCCTGATGATACTG 3064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3106 CCACTTGCTGAGTATGTCGTTAGGACATTCACCTTGGAAAGGAGGGGGCTA 3155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3306 TGGTGCTGGCGCACAGGCTGTTACATTGTTATTGACATAATGCTGGACA 3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3394 GIGAAAGCCTTACGAICTCGGCGCATTAATATGGTACAGACAGAGGAACA 3443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||:::|||
1865 CAACTACATCGACATTIGGCTGTACAGGGAIGGCTACCAGAGACCAAGCC 2914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3356 TGGCTGAAAGAGAGGGTGTGGTT......GACATCTACAACTGT 3393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 laTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAspPheTrp 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 ArgMetIleTrpGluTyrSerValLeuIleIleValMetAlaCysMetGl 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 luMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGluLys 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....PheLys...ArgGlnMetAspVallleArg 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aAsnPheIle......LysGlyValTyrGlyProLysA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 LysGluGluPheAlaAsnGluPheLeuLysLeuLysArgGlnSerThrLy
                                                                                                                                                                        37 sTyrLysAlaAspLysThrTyrProThrThrValAlaGluAsnAlaLysA
                                                                                                                                                                                                                                                                                            54 snlleLysLysAsnArgTyrLysAspIleLeuProTyrAspTyrSerArg
                                                                                                                                                                                                                                                                                                                                                                                                          71 ValGluLeuSerLeuIleThrSerAspGluAspSerSerTyrIleAsnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 uTyrGluMetGlyLysLysCysGluArgTyrTrpAlaGluProGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 ArglysSerAspTyrIleIleArg.....ThrLeuLysValLysPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 nSerGluThrArgThrIleTyrGlnPheHisTyrLysAsnTrpProAspH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 isAspValProSerSerIleAspProIleLeuGluLeuIleTrpAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 ArgCysTyrGlnGluAspAspSerValProIleCysIleHisCysSerAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3256 AAGCTATCTAACCCTCCCAGTGCTGGGCCCATTGTCGTACACTGCAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 etLeuLeuLysAspGlyIleIleProGluAsnPheSerValPheSerLeu
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Align seg 1/1 to: US-08-087-244A-3 from: 1 to: 4374
                                                                                                                 2698 AAAGAGGAATACGAGAGCTTCTTT.
                                                                                                                                                                                                                                  2739 TTGG.....
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d CTGCCATCCCTGTGTGAATTTAAAGCTGCATATTTTGATATGGTAGGA 0	CTGCATATTTTGATATGATTCGA 3543	SerGlyThrGluSerGlnAlaLy 310 CTCAAAGATGAATTTCAGACTCT 3593	TGAAGACTGCAGCATAGCCTGCC 3643	AlaAspSerTyrSerPro 327 GTTTCATGATAGCTCCCACCT 3690	LysalaalaLysMetMetAsnGl 342 :::::: ATGATGGGGAGAGCAGTAACTA 3740	eLysGluSerSerSerPheAspP 357 ::::: :::::::::::::::::::::::::::::::	luGluLeuValLeuHisProAla 373 ::: :::ATGGTCACACAATACCCA 3804	GlubeuasnTyrserPhe 388 ::: ::::: AGATTAGTATATGATTACGGATG 3854	.AspLysasnalaaspThrThrM 396 ::: GGACCTGTCTCAGGGCTGCCCAC 3904	ProllevalGlyGlu 408 	LeuGlySerLeuLeuPheGluGl 425 :: :: :: :: GTGATCAATCTATTAGAAT 4004	
	3494 CTGCCATCCCTGTGTGTAAATTTAAAGCTGCATATTTTGATATGATTCGA	300AspLysHisSerGlyThrGluSerGlnalaLy 11	310 sHisCysI 3594 GAATTCGGTCACCCTCGACTACAAGCTGAAGACTGCAGCATAGCCTGCC	313 leproGluLysasnHisThrLeuGlnAlaaspSerTyrSerPro :: ::: 3644 TGCCAAGGAACCATGACAAGAACCGTTCATGATATGCTCCCACCT	328 ASDLeuProLysSerThrThrLysAlaalaLysMetMetAsnGl ::	342 nGlnArgThrLysMetGluIleLysGluSerSerSerPheaspP	357 heArgThrSerGluIleSerAlaLysGluGluLeuValLeuH18ProAla ::: ::: ::: 3787ATCGTCACACAATACCCA	374 LysSerSerThrSerPheAspPheLeuGluLeuAsnTyrSerPhe ::: :::	389385 TACCTCCATCGTGATGCTAAATGAAGT	396 etLysTrpGlnThrLysAlaPheProIleValGlyGlu :	409 ProLeuGlnLysHisGlnSerLeuAspLeuGlySerLeuLeuPheGluGl 	425 yCysSerAsnSerLysPro 431

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Sequence 2356 BP; 750
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                                                                                                                                                                                                                                                 AAX90696;
                                                                                                                                                                                                                                                 Sequence (Strost Group Carlo C
                                                                                                                                                                     /net/abss06/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA1995.DAT:AAQ94311 + /net/abss06/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2001A.DAT:AAF26466 + /net/abss06/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2001A.DAT:AAF26469 +
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                                                                                        About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
    out_format :
OM of: US-09-600-358A-4 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database length: 858457221
Search time (sec): 351.650000
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Query length: 692
Database: N_Geneseq_032802:*
Database sequences: 1736436
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                                            Date: May 26, 2002
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seq_name: /net/abss06/S1DS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAX90696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lymphoid Protein Tyrosine Phosphatase gene; Lyp gene; immunosuppressant; intracellular tyrosine phosphatase; PrPase; lymphocyte; fetal liver; resting lymphoid cell; protein tyrosine kinase; PTKs; transgenic animal; lymphoma; T cell antigen receptor signalling; intronic sequence; cytokine receptor signalling; protein tyrosine phosphatase; PTPase; ds.
/net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/Na1998.DAT:AAV05762 + Anet/abss06/SIDS1/gcgdata/hold-geneseq-geneseqn-embl.Na1999.DAT:AAV81897 + Anet/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/Na1994.DAT:AAV81897 + Anet/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/Na1994.DAT:AAV81842 + Anet/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/Na2001a.DAT:AAF26467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Cytoplasmic phosphatase Lyp2, cDNA
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P-PSDB; AAY28653.
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1141 1241 1391 1441 1641 1191 517 384 euAsnTyrSerPheAspLysAsnAlaAspThrThrMetLysTrpGlnThr 400 467 534 550 1642 AAAATCCTTATTTTCATCATGGCCTCCAAGTGGTACCAGTTCTAAGATG 1691 367 uLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuGluL 384 417 434 laAlaGlyArgTyrPheAsnSerLysValProlleThrArgThrLysSer 450 484 luMetGlnAlaGlnLysValMetHisValSerSerAlaGluLeuAsnTyr 500 300 941 317 991 284 891 yrAsnAlaValLeuGluLeuPheLysArgGlnMetAspValIleArgAsp 1092 GAATCTTCTTCCTTTGACTTTAGGACTTCTGAAATAAGTGCAAAAGA 1142 GCTAGTTTTGCACCCTGCTAAATCAAGCACTTCTTTTGACTTTCTGGAGC luAsnProTyrPheSerSerTrpProProSerGlyThrSerSerLysMet GGGATAATTCCTGAGAACTTCAGTGTTTTCAGTTTGATCCGGGAAATGCG gThrGlnArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValT 1192 TAAATTACAGTTTTGACAAAAATGCTGACACACCATGAAATGCCAGACA 401 LysAlaPheProIleValGlyGluProLeuGlnLysHisGlnSerLeuAs 451 ThrProPheGluLeuIleGlnGlnArgGluThrLysGluValAspSerLy SerLeuProTyrAspSerLysHisGlnIleArgAsnAlaSerAsnValLy 351 GluSerSerPheAspPheArgThrSerGluIleSerAlaLysGluGl 367 501 534 267 892 792 842 284

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alignment_scores:
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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:AAX90695
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/product= "Cytoplasmic phosphatase, Lyp 1"
/note= "Expressed in thymocytes, mature T and
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                                                                                                                                                   1892 ACTTCCTGTACGGACACCTGAATCATTTATTGTGGTTGAGGAAGCTGGAG 1941
                                                                                                                                                                                              1942 AATTCTCACCAAATGTTCCCAAATCCTTATCCTCAGCTGTGAAGGTAAAA 1991
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                                                                                           uLeuProThrSerThrSerLeuPheSerTyrTyrAsnSerHisSerS
                                                   erLeuSerLeuAsnSerProThrAsnIleSerSerLeuLeuAsnGlnGlu
                                                                                                                                         oLeuProValArgThrProGluSerPheIleValValGluGluAlaGlyG
                                                                                                                                                                                  luPheSerProAsnValProLysSerLeuSerSerAlaValLysValLys
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ID AAX90695 standard; cDNA; 3058
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P-PSDB; AAY28652.
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      267
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The present cDNA sequence is that of the Lymphoid Protein Tyrosine
Phosphatase gene, Lyp 1 that encodes a cytoplasmic tyrosine phosphatase
protein with a single catalytic domain. The Lyp gene has been localised
to human chromosome lpl3: It is expressed in the lymphoid cells,
particularly in thymocytes, mature B and T cells. It is involved in
lymphocyte growth and development. Lyp gene products are important for
regulation of T cell antigen and cytokine receptor signalling and early
and late stages of T cell differentiation. Lyp 1 has immunosuppressive
cutivity. This sequence is used to treat lymphoma, to reduce or prevent
T cell activation or proliferation and to control thymocyte
differentiation. Fragments of this gene are used, as probes or primers,
to identify allelic variations and for dispnosis of diseases associated
with reduced Lyp activity. Transgent animals in which a Lyp gene has
been inactivated or replaced by a heterologous Lyp gene are used to
New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signalling through T cells, particularly as immunosuppressant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 TTATAGCCGGGTAGAACTATCCCTGATAACCTCTGATGAGGATTCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 685
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             study and screen for possible therapeutic agents.
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                                                                                                     Claim 5a; Page 52; 105pp; English
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Ratio: 5.216
Percent Similarity: 100.000
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US-09-600-358A-4 x AAX90695
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1191
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CTGGAATTTGGCCCTTTCTCTGTATCCTGTGAAGCTGAAAAAGGAAATC
                                                                         hrIleTyrGlnPheHisTyrLysAsnTrpProAspHisAspValProSer
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534 luAsnProTyrPheSerSerTrpProProSerGlyThrSerSerLysMet 1642 AAAATCCTTATTTTTCATGGCCTCCAAGTGGTACCAGTTCTAAGATG uLeuProThrSerThrSerLeuPheSerTyrTyrAsnSerHisSerS 1792 CTTTATCACTGAATTCTCCAACCAATATTTCCTCACTATTGAACCAGGAG 1992 ATTGGAACATCACTGGAATGGGGTGGAACATCTGAACCAAAGAAATTTGA sGluAsnPheSerTyrLeuGluSerGlnProHisAspSerCysPheValG 584 erLeuSerLeuAsnSerProThrAsnIleSerSerLeuLeuAsnGlnGlu SerAlaValLeuAlaThrAlaProArgIleAspAspGluIleProProPr 634 luPheSerProAsnValProLysSerLeuSerSerAlaValLysValLys IleGlyThrSerLeuGluTrpGlyGlyThrSerGluProLysLysPheAs pAspSerVallleLeuArgProSerLysSerValLysLeuArgSerProL SerLeuProTyrAspSerLysHisGlnIleArgAsnAlaSerAsnValLy SerLeuAspLeuProGluLysGlnAspGlyThrValPheProSerSerLe 484 luMetGlnAlaGlnLysValMetHisValSerSerAlaGluLeuAsnTyr 2092 AATCA 2096 ysser 685

seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/nA1999.DAT:AAV81742 seq_documentation_block
ID AAV81742 standard;

BP

CDNA;

standard;

AAV81742;

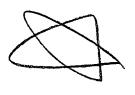
(first entry) 10-MAR-1999 encoding cDNA PTP04 Human

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease; ss.

153 AATCTACCAAGTACAAGGCAGACAAAACCTATCCTACAACTGTGGCTGAG

S

New nucleic acid encoding specific protein tyrosine phosphatases useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease Jallal B; App H, Clary D, Courtneidge SA, Hui TH, Markby D, Onrust S, Peles E, Plowman GD; Claim 2; Page 145-146; 193pp; English Location/Qualifiers 53..2476 /*tag= a 97US-0047222. 97US-0049477. 97US-0049756. 97US-0049914. 97US-0063595 97US-0044428 98WO-US08439 WPI; 1999-009434/01 (SUGE-) SUGEN INC. P-PSDB; AAW89247 Homo sapiens WO9849317-A2 27-APR-1998; 23-OCT-1997; 28-APR-1997; 20-MAY-1997; 11-JUN-1997; 11-JUN-1997; 05-NOV-1998 18-JUN-1997 Key



The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The resent sequence encodes human PTP04. The above proteins. The present sequence encodes human PTP04. The above proteins. There is the resent sequence encodes human PTP04. The above proteins, other than a LK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and humans), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzhahemr's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynuclectides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in generate therapy (optionally after mutation). Ab are used to determine the proteins.

Sequence 3580 BP; 1213 A; 666 C; 618 G; 1083 T; 0 other;

Gaps: 1 Percent Identity: 99.416 Length: Quality: 3543.50 Ratio: 5.188 Harity: 99.708 US-09-600-358A-4 x AAV81742 Ratio: Percent Similarity: alignment_scores: alignment_block:

Align seg 1/1 to: AAV81742 from: 1 to: 3580

- 34 lnSerThrLysTyrLysAlaAspLysThrTyrProThrThrValAlaGlu 50

	snalalysasnilelyslysasnarqTyrLysaspileLeuProTyrA :: acccaagaaTaTCaaGaAaAaCaGaTATAAGGATATTTGCCCTATG TyrSerArgValGluLeuSerLeuIleThrSerAspGluaspSerSer
TTATA(SCGGGTAGAGGGGTGGGTGGGTGGGGGGGGGGGGGGGGGG
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eTrp(TTGG(GlutyrSerValLeuileileValMetAlaCysMetGlutyrGlum 134
etG] TGGG	yLysLysLysCysGluargTyrTrpAlaGluProGlyGluMetGln 150
LeuG	lupheGlyProPheSerValSerCysGlualaGluLysArgLysSe 167
rAsp TGAT	TyrileileargthriæuLysValLysPheasnSerGluThrargT 184
hril 	IleTyrGlnpheHisTyrLysAsnTrpProAspHisAspValProSer 200
Ser	IleaspProlleLeuGluLeuIleTrpaspValargCysTyrGlnG 217
uAs - - GGA	PASPSerValProlleCyslleHisCysSerAlaGlyCysGlyArgT 234
hrG CTG	1yValileCysAlaileValAspTyrThrTrpMetLeuLeuLysAsp 250
G13 	IleIleProGluAsnP
gThr(GACA(rGlnargProSerLeuValGlnThrGlnGluGlnTyrGluLeuValT 284
yra 	AsnalavalleuGluLeuPheLysargGlnMetAspvallleargAsp 300
Lys] - - AAA(HisSerGlyThrGluSerGlnAlaLysHisCysIleProGluLysAs 317
nHis -	SThrLeuGlnAlaAspSerTyrSerProAsnLeuProLysSerThrT 334
hrLy CAAA	salaalaLysMetMetAsnGlnGlnArgThrLysMetGlulleLys 350

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1700 TCTCTTGATTTACCTGAGAAGCAAGATGGAACTGTTTTTCCTTCTTCTT 1749
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                    1150 GCTAGTTTTGCACCCTGCTAAATCAAGCACTTCTTTTGACTTTCTGGAGC
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351 GluSerSerPheAspPheArgThrSerGluIleSerAlaLysGluGl
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                                                                     uLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuGluL
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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAH79342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of human tyrosine phosphatase hPTP. The protein is expressed in human normal suprarenal tissue. The present sequence is the coding sequence of the
                          2049
                                                                  Human protein tyrosine phosphatase and its coding sequence
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pAspSerValIleLeuArgProSerLysSerValLysLeuArgSerProL
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Gaps: 11
Percent Identity: 89.229
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                                                                                                                                                                                                                                                                                    Human tyrosine phosphatase coding sequence
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ID AAH79342 standard;
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	51 AsnalalysasnIleLysLysAsnargTyrLysAspIleLeuProTyrAs :::	67 pTyrSerArgvalGluLeuSerLeuileThrSerAspGluAspSerSerT 	84 yrlleasnalaasnPhelleLysGlyValTyrGlyProLysalaTyrIle 	101 AlaThrGlnGlyBroLeuSerThrThrLeuLeuAspPheTrpArgMet11 	117 eTrpGluTyrSerValLeuIleIleValMetalaCysMetGluTyrGluM 	134 etGlyLysLysLysCysGluArgTyrTrpAlaGluProGlyGluWetGln 	151 LeuGluPheGlyProPheSerValSerCysGluAlaGluLysArgLysSe 	167 raspīyrīleileargīhrīeulysvallysPheasnSerGluThrargī 	184 hrlletyrglnPheHisTyrLysAsnTrpProAspHisAspValProSer 	201 SerileAspProlleLeuGluLeuileTrpAspValArgCysTyrGlnGl 	217 uAspAspSerValProlleCys1leHisCysSerAlaGlyCysGlyArgF 	234 hrGlyValIleCysAlaIleValAspTyrThrTrpMetLeuLeuLysAsp 	51 GlylleileprogluasnPheSerValPheserLeuileargGlumetar 	267 gThrGlnArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValT 	84 yrasnalavalLeuGluLeuPheLysArgGlnMetaspVallleArgAsp 	301 LysHisserGlyThrGluSerGlnAlalysHisCysIleProGluLysAs 	317 nHisThrLeuGlnalaAspSerTyrSerProAsnLeuProLysSerThrT 	34 hrLysAlaAlaLysMetMetAsnGlnGlnArgThrLysMetGluIleLys
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1007 CAAAAGCAGCAAAAATGATGAACCAACAAAAGGACAAAAATGGAAATCAAA 1056 1431 1830 1245 GAATTGGGCCTCTTTTGTTTAGGAATGTCTA...ATTCTAACCTTGTAT 1291 1581 1681 1781 400 533 417 467 1482 TTCACTGCCATATGACTCTAAACACCAAATACGTAATGCCTCTAATGTAA 1531 384 500 517 550 567 583 9 617 yGluPheSerProAsnValProLysSerLeuSerSerAlaValLysValL 650 467 ysGluAsnPheSerTyrLeuGluSerGlnProHisAspSerCysPheVal 483 GluSerSerSheAspPheArgThrSerGluIleSerAlaLysGluGl uLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuGluL euAsnTyrSerPheAspLysAsnAlaAspThrThrMetLysTrpGlnThr LysAlaPheProlleValGlyGluPro.LeuGlnLysHisGlnSerLeuA 417 spLeuGlySerLeuLeuPheGluGlyCysSerAsnSerLysProValAsn 434 AlaAlaGlyArgTyrPheAsnSerLysValProlleThrArgThrLysSe 450 rThrProPheGluLeuIleGlnGlnArgGluThrLysGluValAspSerL 484 GluMetGlnAlaGlnLysValMetHisValSerSerAlaGluLeuAsnTy rSerLeuProTyrAspSerLysHisGln1leArgAsnAlaSerAsnValL 534 GluAsnProTyrPheSerSerTrpProProSerGlyThrSerSerLysMe 550 tSerLeuAspLeuProGluLysGlnAspGlyThrValPheProSerSerL uSerAlaValLeuAlaThrAlaProArgIleAspAspGluIleProProP ysHisHisAspSerSerAlaLeuGlyValTyrSerTyrIleProLeuVal euLeuProThrSerSerThrSerLeuPheSerTyrTyrAsnSerHisSer 584 SerLeuSerLeuAsnSerProThrAsnIleSerSerLeuLeuAsnGlnGl 351 200 517 009 633 367 384 401 267

to: 2983

from: 1

to: ABI99910

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US-09-600-358A-4 x ABI99910
   alignment_block:
                                                      Align seg 1/1
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                                                                                                                                                                                                                  seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:AB199910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia or vasospaatic ischaemia) by measuring the protein sequences in ABB57020 to ABB57374) or by determining the expression levels of particular genes (ABI99202 to ABB99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes a method for examining ischaemic
                                                                                                                                                                                                                                                                                                                                                                               Mouse ischaemic condition related cDNA sequence SEQ ID NO:1063
                                                                   Ishii Y;
650 yslleGlyThrSerLeuGluTrpGlyGlyThrSerGluProLysLysPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2983 BP; 923 A; 634 C; 681 G; 745 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 2680-2685; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi Y,
                                                                                                                                                                                                                                                                    ABI99910 standard; cDNA; 2983 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8-MAY-2000; 2000JP-0145977
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Quality: 1104.50
Ratio: 2.493
.....arity: 59.623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-034733/04.
P-PSDB; ABB57374.
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                                                                                                                                                                                                                                                                                                          ABI99910;
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                                                                                                                                           683
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Length: 743
Gaps: 22
Percent Identity: 35.935

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130 etGluTyrGluMetGlyLysLysLysCysGluArgTyrTrpAlaGluPro 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651
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                                                                                                                                     46
                                                                                                                                                                                                                                                                                                                                             80 luAspSerSerTyrIleAsnAlaAsnPheIleLysGlyValTyrGlyPro 96
                                                                                                                                                                                                                                                                                                                                                                               302 AAGATTCAGATTATATCAATGCAAATTTTATTAAGGGTGTGTATGGGCCA 351
                                                                                                                                                                                                                                                                           eLeuProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAspG 80
230 lyCysGlyArgThrGlyValileCysAlaileValAspTyrThrTrpMet
                                                                                                                                   799 TTACTGAAAGCAGGGAAAATTCCAGAGGAATTTAATGTATTTAATTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                    452 GAGAATTTGAGATGGGAAGGAAAAAGTGTGAGCGCTACTGGCCTTTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||| ::: |||||||| || 502 GGGGAGGATCCTATAAAATTTCTTGTGAAAATGA
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                                                                   17 sLysileThr...
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280	yrGluLeuValTyrAsnAlaValLeuGluLeuPheLysArgGlnMetAsp ::::: ::: ATGAACTTGTTCATAGGGCTATTGCTCAACTGTTTGAAAACAGCTACAAC	296 948
297	Valile	298
949	TGTATGAAATTCATGGAGCACAGAAGATCCGTGATGGTAATGAAATTACC	866
299	ACTGGAACTATGGTCCATTGATAGCGAGACGAGACTCTCCGCCA	303 . 1048
304	The Glythe	305
1049	 AAGCCGCCGCGGACTCGAAGTTGCCTTGTAGAAGGGGGATGCCAAGGAAGA	1098
306	GluSerGlnalaLysHisCysIleProGluLysAsnHisThrLeuGlnal::::: :::	322 1148
322	aAspSerTyrSerProAsnLeuProLysSerThrThrLysAlaAlaLysM ::	339 1192
339	etMetAsn	341
342	IGACAGGITACCACCCAAAGCCAGIGCIGCACIGGCCICACCAGAGGCAAC GinginarafhtiwaMatGiufiaIwgGingorgargargabaaanbaa	1242
4 4	ACCAGGCGACCTCAACAGAAGCTATGATAAATCAGGG	336 1280
358 1281	gThrSerGluIleSerAlaLysGluGluLeuValLeuHisProAlaLysS 	375 1297
375 1298	erSerThrSerPheAspPheLeuGluLeuAsnTyrSerPheAspLysAsn ::::::::::::::::::::::::::::::::::	391 . 1329
392	AlaaspThrThrMetLysTrpGlnThrLysAlaPheProIle	405 1379
405		405
1380	GCCCAAAAGTTTTGATGGGAACACACTCTTGAATAGGGGACATGCGATTA	1429
406		414 1479
415	SerLeuAspLeuGlySerLeuLeuPheGluGlyCysSerAsnSerLysPr:: ::: ::::: :::	431 1529
431	oValasnalaalaglyargtyr	438
439	PheAsnSerLysValProlleThrArgThrLysSerThrPro 	452 1626
453	PheGluLeuIleGlnGlnArgGluThrLysGluValaspSerLysGluAs :::::	469 1673
469	nPheSerTyrLeuGluSerGlnProHisAspSerCysPheValGluMetG 4 :: :: :: :: :: :: : : : : : : : : :	486 1720

	486 InAlaGlnLysValMetHisValSerSerAlaGluLeuAsnTyrSerLeu 502
	::::: :::
	503 ProTyrAspSerLysHisGlnIleArgAsnAlaSerAsnValLysHisHi 519
	::::: ::::: ::::::
	519 sAspSerSerAlaLeuGlyValTyrSerTyrIleProLeuValGluAsnP 536 ::: 1800 CAACAGCTCC
	536 roTyrPheSerSerTrpProProSerGly 545
	546 ThrSerSerLysMetSerLeuAspLeuProGluLysGlnAspGlyThrVa 562 1876 GGGAGCTCTGATGGTGCTGT 1895
	562 lPheProSerSerLeuLeuProThrSerSerThrSerLeuPheSerTyrT 579
	579 yrAsnSerHisSerSerLeuSerLeuAsnSerProThrAsnIleSerSer 595 ::: ::: ::: :: ::
	596 LeuLeuAsnGlnGluSerAlaValLeuAlaThrAlaProArg 609 ::: :::
	610IleAspAspGluIJeProProLeuProValA 621
	621 rgThrProGluSerPheileValValGlu 630
-bəs	eq_name: /net/abss06/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2000.DAT:AAF21801
seg_ ID	documentation_block: AAF21801 standard; DNA; 1286 BP.
X X	AAF21801;
¥ E \$	27-MAR-2001 (first entry)
SE S	Human breast and ovarian cancer associated antigen gene SEQ ID 188.
K K K K K K K K K K K K K K K K K K K	Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuncer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
80 SO	Homo sapiens.
X d	WO200055173-A1.
X G S	21-SEP-2000.
AA YX	08-MAR-2000; 2000WO-US05881.
PR	12-MAR-1999; 99US-0124270.
PA XX	(HUMA-) HUMAN GENOME SCI INC,
PI	Rosen CA, Ruben SM;

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proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22040 and AAB59129 which are used in the sequences AAF22040 and AAB59129 which are used in the sequences AAF22040 and AAB59129 which are used in the invention and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antivital; antialergic; hepatotropic; antidiabetic; antiinflammatory; antialergic; hepatotropic; antidiabetic; antiinflammatory; antialergic; hepatotropic; antidiabetic; antiinflammatory; antibores; so antidiabetic; antiportial; antiporasis of cancer. The nucleic acid sequences, particularly breast and ovarian cancer. The nucleic acid sequences, particularly breast and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crooh's disease, multiple sclerosis, rheumatoid myocardial ischaemias; wound healing; neurological diseases such as myocardial anoxia and epilepsy; and infectious diseases.
                                                                                       New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 H1sAspSerCysPheValGluMetGlnAlaGlnLysValMetHisValSe 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 TTCAGCAGAACTGAATTATTCACTGCCATATGACTCTAAACACCCAAATAC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAATGCCTCTAATGTAAAGCACCATGACTCTTAGTGCTCTTGGTGTATAT 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rgAsnAlaSerAsnValLySHiSHiSAspSerSerAlaLeuGlyValTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CATGATICTTGTTGTAGAGGATGCAGGCTCAAAAAGTAATGCATGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1286 BP; 410 A; 273 C; 209 G; 389 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 208
Gaps: 0
Percent Identity: 99.038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAF21801 from: 1 to: 1286
                                                                                                                                                                                                            Claim 1; Page 622; 1299pp; English.
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99.519
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                     2000-611515/58
                                           P-PSDB; AAB58898
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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:AAV17097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This cDNA clone codes for a novel rat protein tyrosine phosphatase, designated PTP20 (see AAW49906), that regulates growth factor stimulation of cellular differentiation. The clone was isolated

    useful in the diagnosis and

                                                                                                                                                                                                                                                                                                                                                                                                   PTP20; rat; signal transduction; neural injury; therapy; ss.
                                                                                                         501
                                                                                                                                661
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627
                                                                                644
                                                         402 ATGATGAATCCCCCCCCCCTCCTGTACGGACACCTGAATCATTTATT 451
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                                                                                              644 rSerAlaValLysValLysIleGlyThrSerLeuGluTrpGlyGlyThrS
                                                                                                                                            661 erGluProLysLysPheAspAspSerValIleLeuArgProSerLysSer
                                                                                                                                                                                          628 ValValGluGluAlaGlyGluPheSerProAsnValProLysSerLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nayler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim YW,
                                                                                                                                                                                                                                                                                                                                                                              Rat protein tyrosine phosphatase PRP20 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of signal transduction disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New phosphatase and kinase enzyme(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
28..1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig la-b; 138pp; English.
                                                                                                                                                                                                                                          602 GTAAAACTCCGAAGTCCTAAATCA 625
                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                             678 ValLysLeuArgSerProLysSer 685
                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAV17097 standard; cDNA; 2226
                                                                                                                                                                                                                                                                                                                                                                                                     Protein tyrosine phosphatase; cell differentiation; cancer;
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96US-0019629.
96US-0023485.
96US-0030860.
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2150..2156
/*tag= b
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using primers based on consensus sequences (see AAW49915-16) of known PTPs. The invention relates to novel proteins (see AAW49915-16) of known involved in cellular signal transduction and to the nucletc acids (see AAV17097-99) coding for them, and provides vectors, host cells, purified recombinant proteins, methods for identifying compounds that bind the novel proteins or abrogate their interactions with natural binding partners, as well as methods for the diagnosis and treatment of diseases associated with the novel proteins. For PTP20, activators may act as anti-cancer therapeutics that stimulate cell differentiation rather than proliferation, while inhibitors may be useful for treating neural injuries by delaying the differentiation of transplanted neuronal stem cells until they are firmly grafted.
from a rat phaeochromocytoma PC12 cDNA library by PCR amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 hrileTyrGlnPheHisTyrLysAsnTrpProAspHisAspValProSer 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 AlaLysAsnIleLysLysAsnArgTyrLysAspIleLeuProTyrAspTy
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                                                                                                                                                                                                                                                                                           Sequence 2226 BP; 574 A; 591 C; 604 G; 457 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 7
Percent Identity: 43.137
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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAV03112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-receptor protein tyrosine phosphatase; hematopoietic stem cell; pry HSC, progenitor cell; tyrosine phosphatase domain; PTP HSC agonist; tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist; stem cell differentiation; s.y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding a novel non-receptor tyrosine phosphatase.
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                                                                                                   CAGACAATCCCACCCAATTTCAGCCTCTTTGAAGTGGTCCTGGAGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                      302 sSerGlyThrGluSerGlnAlaLysHisCysIleProGluLysAsnHisT
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634 AGTICCGAICACATICICACCAIGGIGGAGGAGGCCCGTIGCCICCAAGG
                                                                                                                                         hrGlyValIleCysAlaIleValAspTyrThrTrpMetLeuLeuLysAsp
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                                                                                      uAspAspSerValProlleCysIleHisCysSerAlaGlyCysGlyArgT
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The present sequence encodes a novel murine non-receptor protein tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein is protein is prodeminantly expressed in early hematopoietic stem cells (HSCs) or predominantly expressed in early hematopoietic stem cells (HSCs) or progenitor cells, and lack expression in adult tissues. The protein has a N-terminal tyrosine phosphatase domain, followed by a region rich in serine, threonine and proline and a C-terminal region of about 15-25 amino acids which is rich in basic amino acid residues. The protein is capable of tyrosine dephosphorylation in hematopoietic progenitor cells, and functional derivatives of such native tyrosine phosphatases. The phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or progenitor cell can be used in an assay for the identification of PTP HSC or andifferentiated malignant hematopoietic cells, e.g. leukaemia cells, which may facilitate their hematopoietic cells, e.g. leukaemia cells, which may facilitate their treatment. The PTP HSC or an agonist antibody against the PTP HSC or an agonist the PTP HSC can be used for the expansion of undifferentiated stem cells in cell culture can be appeared by the contraction of the expansion of undifferentiated stem cells in cell culture can be used for the expansion of the contraction of t
                                                                                                                                                                                                                                                                                                                                         Hematopoietic stem cell non-receptor protein tyrosine phosphatase - useful for expansion of undifferentiated stem cells in cell culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marrow transplantation), while the agonist antibody along with a hematopoietic growth factor can be used for the expansion of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 AGTCATCCTTTCCCTGCTCCAAGAGGAGGGACATGGAAATTACATCAATG 283
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Gaps: 6
Percent Identity: 44.037
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US-09-600-358A-4 x AAV03112
(GETH ) GENENTECH INC
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                                                                                                 Cheng J, Lasky LA;
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GlyProLeuSerThrThrLeuLeuAspPheTrpArgMetIleTrpGluTy 120

284 CCAACTTCATCCGGGGCATAGATGGAAGCCAGGCCTACATTGCGACGCAA

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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:AAV17099
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                                                                                               154 GlyProPheSerValSerCysGluAlaGluLysArg...LysSerAspTy 169
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120 rSerValLeulleIleValMetAlaCySMetGluTyrGluMetGlyLysL 137
                  384 TGGGGTCAAGGTAATCCTGATGGCCTGTCAAGAGACAGAAAATGGACGGA
                                                                           ysLysCysGluArgTyrTrpAlaGluProGlyGluMetGlnLeuGluPhe
                                                                                                                                                                                           GGGCCTTTCTGCATCACCCTGACAAAGGAGACAACACTGAATGCAGACAT
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therapy; diagnosis; ss.
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ID AAV17099 standard; cDNA; 2810
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                                                                           137
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AlaAsnGluPheLeuLysLeuLysArgGlnSerThrLysTyrLysAlaAs

25

41

13

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This cDNA sequence codes for a novel human protein tyrosine phosphatase (PTP), designated brain derived phosphatase 1 (BDP-1, see AAW49908), that is expressed in most tissues and cell lines at basal level, but expressed high in epithelium origin cell lines and cancer cell lines. BDP-1 was originally identified in a human brain cDNA library, although the full-length clone was isolated from the haematopoietic MEG01 CDNA library. The invention relates to novel proteins (see AAW49906-14) involved in cellular signal transduction and to the nucleic acids (see AAV17097-99) coding for them, and provides vectors, host cells, purified recombinant proteins, methods for identifying compounds that activate or inhibit the novel proteins, as well as methods for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New phosphatase and kinase enzyme(s) - useful in the diagnosis and treatment of signal transduction disorders
'note= "GC-rich track, part of Kozak sequence"
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        44...1420
**tag= b
**transl_except= (pos:69..71, aa:Arg)

*transl_except= (pos:162..164, aa:His)

**transl_except= (pos:1182..1184, aa:Ser)
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                                                                                                                                                           /.rag= e
/note= "site of 91 bp intron"
2532..2545
/*tag= f
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/note= "site of 367 bp intron'
799
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                                                                                                                                                          'note= "site of 80 bp intron'
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96US-0023485.
96US-0030860.
96US-0030964.
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Ullrich A, Wang HY;
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291

Length: Gaps:

708.00 3.218 75.601

Quality: Ratio:

alignment_scores:

Percent Similarity:

Percent Identity: 46.735

Align seg 1/1 to: AAV17099 from: 1 to: 2810

US-09-600-358A-4 x AAV17099

alignment_block:

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518
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                       172 CGCCGTGTCCTCCACCGTGGCCGGCAGAGAACGTGAGAAGA 221
                                                                                       271
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                                                                                                                                                                                                                                                            240 eValAspTyrThrTrpMetLeuLeuLysAspGlyIleIleProGluAsnP
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                                                                                                                                                                                 sGlyValTyrGlyProLysAlaTyrIleAlaThrGlnGlyProLeuSerT
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519 TCACTCTGATAAAGGAGAAGTGGCTGAATGAGGACATCATGCTCAGGACC
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41 pLysThrTyrProThrThrValAlaGluAsnAlaLysAsnIleLysLysA
                                                                                                                       LeuIleThrSerAspGluAspSerSerTyrIleAsnAlaAsnPheIleLy
                                                                                                                                                                                                                                                                                                                                                                                                                             158 alSerCysGluAlaGluLys...ArgLysSerAspTyrIleIleArgThr
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31 uLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThrThrV

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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1998.DAT:AAV71076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein tyrosine phosphatase 1C-green fluorescent protein fusion product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimera; ss
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:::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :
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Gaps: 27
Percent Identity: 26.728
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ID AAV71076 standard; cDNA; 2562
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Chimeric - Homo sapiens.
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54.531
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US-09-600-358A-4 x AAV71076
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P-PSDB; AAW85031.
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Percent Similarity:
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                                                                                                                                                                                                                                                           AAV71076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1194 GGTCTCCCCGCTGGACAATGGAGACCTGATTCGGGAGATCTGGCATTACC 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1294 CTCAGCTTCCTGGACCAGATCAACCAGCGGCAGGAAAGTCTGCCTCACGC 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175
                                                                                                                                                                                                                                                                                                                                        ro.........LysAlaTyrIleAlaThrGlnGlyProLeuSerThr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 eValMetAlaCysMetGluTyrGluMetGlyLysLysLysCysGluArgT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158
                                                                                                                                                                                              896
                                                                                                                                                                                                                                                                                                                                                                      109 ThrLeuLeuAspPheTrpArgMetIleTrpGluTyrSerValLeuIleIl 125
......AACTTGCACCAGCGTCTGG 796
                                                                                               797 AAGGGCAGCGGCCAGAGAACAAGGGCAAGAACCGCTACAAGAACATTCTC 846
                                                  64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1047 CGTCATGACCACCCGAGAGGTGGAGAAAGGCCGGAACAAATGCGTCCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 yrTrpAlaGluProGlyGluMetGlnLeuGluPheGlyProPheSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1097 ACTGGCCCGAGGTGGGC...ATGCAGCGTGCTTATGGGCCCTACTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerCysGluAlaGluLysArgLysSerAspTyrIleIleArgThrLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1144 ACCAACTGCGGGGAGCATGACAACCGAATACAAACTCCGTACCTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 sValLys.....PheAsnSerGlu...ThrArgThrIleTyrGlnPheH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isTyrLysAsnTrpProAspHisAspValProSerSerIleAspProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGluLeuIleTrpAspValArgCysTyrGlnGluAsp.....AspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 rValProlleCyslleHisCysSerAlaGlyCysGlyArgThrGlyValI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 leCysAlaIleValAspTyrThrTrpMetLeuLeuLysAspGlyIleIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1394 TCATTGTCATC.....GACATGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....IleArgGluMetArgThrGlnArgProSerLeuValGlnThrGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 luGlnTyrGluLeuValTyrAsnAlaVal.....LeuGluLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysArgGlnMetAspVallleArgAspLysHisSerGlyThrGluSerGl
                                                    48 alAlaGluAsnAlaLysAsnIleLysLysAsnArgTyrLysAspIleLeu
                                                                                                                                                 65 ProTyrAspTyrSerArgValGluLeuSerLeulleThrSerAsp...Gl
                                                                                                                                                                                                                                              80 uAspSerSerTyrIleAsnAlaAsnPheIleLysGly...ValTyrGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 ProGluAsnPheSerValPheSerLeu......
     759 GCAGAAGCAGGAGGTGAAG.
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308	nAlaLysHisCysIleProGluLysAsnHisThrLeuGlnAl	325
1611	GTACGGGAACATCACCT	1627
325 1628	yrSerProAsnLeuProLysSerThrThrLysAlaAlaLys	338 1677
339 1678	AAACACAAGGAGGATGTGTATGAGAACCTGCACACTAAGAACAAGGG	346 · 1727
346 1728	SMCtGluIleLysGluSerSerSerPheAspPheArgThrSerGluIleS : :::: :::	363 1777
363 1778	eralalysglugluLeuValLeuHisPro	372 1827
373	CCACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGT	380 1877
381 1878	GGTGCCCATCCTGGTCGAGCTGGCGCGACGTAAACGGCCACAAGTTCA	389 1927
389 1928	splysasnalaasp	393 1977
393		393
1978	AAGTICATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGT	2027
394 2028	.ThrThrMetLysTrpGlnThrLysAlaPheprolleValGlyGluProlleValH1!:: :: :: :: :: :: :: :: :: :: :: :: ::	410
410 2078	euGlnLysHisGlnSerLeuAspLeuGlySerLeuLeuPheGluGlyCys::::::	426 2121
427		443 2156
443	IProlleThrArgThrLysSerThrProPheGluLeulleG	457 2206
457	<pre>lnGlnArgGluThrLysGluValAspSerLysGluAsnPheSerTyrLeu :::: </pre>	473 2256
474	GluSerGlnProHisAspSerCysPheValGluMetGlnAl ::::! ::::: ::::: GGGCACAAGCTGGAGTACAACTACAACGCCACAACGTCTATATCATGC	487 2306
487	aGlnLysValMetHisValSerSerAlaGluLeuAsnTyrSerLeuProT ::: ::: ::: ::::::::::::::::::::::	504 2346
504	yrAspSerLysHisGlnIleArgAsnAlaSer	514 2388
515	TACCAGCAGAACACCCCATCGACGCCCGTGCTG.	528 2427
528	ProproserG	545

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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT:AAT06027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Density enhanced Type III receptor-like protein tyrosine phosphatase;
hubEP-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New density enhanced protein tyrosine phosphatase - used to develop prods. to modify transcription, translation and/or activity of tyrosine phosphatase(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Degenerate primers (see AAT06028-29) corresp, to conserved protein tyrosine phosphatase (PTP) amino acid sequences were used to prime a PCR with a HeLa cell cDNA library as template. An isolated clone was used to screen an oligo-dr-primed HeLa cDNA library. A cDNA clone was obtd. (given in AAT06027) that encoded a novel density-enhanced Type III receptor-like PTP, designated hubbP-1 (AAR85203). Expression of the cDNA in host cells allows large-scale prodn. of
545 lyThrSerSerLysMetSerLeuAspLeuProGluLysGlnAspGlyThr 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5117 BP; 1314 A; 1294 C; 1293 G; 1216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 295
Gaps: 7
Percent Identity: 38.305
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350..4363
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAT06027 standard; cDNA; 5117
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2.579
66.780
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US-09-600-358A-4 x AAT06027
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Ratio:
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                                                                                                                                                                                                                                                                                       2500 GTC 2502
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                                                                                                                                                                                                                        562 Val 562
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4139 ACCGTG......GATGTGTATGGGATTGTGTATGACCTTCGAAT 4176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3939 AGTICCATITCACCICCIGGCCAGACCACGGIGIICCCGACACCACIGAC 3988
                                                       3398 AAATCTAAGTTAATCAGAGTGGAGAATTTTGAGGCCTACTTCAAGAAGCA 3447
                                                                                                                                                                            3448 GCAAGCTGACTCCAACTGTGGGTTCGCAGAGGAATACGAAGATCTGAAGC 3497
                                                                                                                                                                                                                                                                                                                                                                                        3548 GGAAAGAATCGCTATAATAATGTTCTGCCCTATGATATTTCCCGTGTCAA 3597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 lLeuIleIleValMetAlaCysMetGluTyrGluMetGlyLysLysLysC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 PheSerValSerCysGluAlaGluLysArgLysSerAspTyrIleIleAr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 gThrLeuLysValLys.....PheAsnSerGluThrArgThrIleTyrG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 lyValIleCysAlaIleValAspTyrThrTrpMetLeuLeuLysAspGly 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 rGlnArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValTyrA 285
                                                                                                                                                                                                                                                                                                                                                                72
15 GlnSerLysLysIleThrLysGluGluPheAlaAsnGluPheLeuLysLe 31
                                                                                                                  31 uLysArgGlnSerThr..........LysTyrLysAlaAspLys. 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3645 ACATGCCTGGCTACCACTCCAAGAATTTTATTGCCACACAAGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3745 ATATGCCATCATTATGTTGACTAAATGTGTTGAACAGGGAAGAACCAAAT
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                                                                                                                                                                                                                                       .....ThrTyrProThrThrValAlaGluAsnAlaLysAsnIle
                                                                                                                                                                                                                                                                                                  3498 ITGITGGAATTAGTCAACCTAAATATGCAGCAGAACTGGCTGAGAATAGA
                                                                                                                                                                                                                                                                                                                                                            56 LysLysAsnArgTyrLysAspIleLeuProTyrAspTyrSerArgValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uLeuSerLeuIleThrSerAspGluAspSerSerTyrIleAsnAlaAsnP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 pAspSerValProIleCysIleHisCysSerAlaGlyCysGlyArgThrG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI58418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nerropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                      nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                            peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qian XB,
Yang Y,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 621; 10078pp; English.
                                                                                                                                                   Human polynucleotide SEQ ID NO 621.
                                                  BP
                                                  4798
                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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                                                                                                                    (first entry)
                                                    CDNA;
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P-PSDB; AAM39262.
                                seq_documentation_block:
ID AAI58418 standard; o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                     WO200153312-A1
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                                                                                                                                                                                                                                                                         Leukaemia; ss
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                                                                                                                                                                                                                                                                                                        Homo sapiens.
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09-JUL-2000;
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                                                                                                                  22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT,
                                                                                   AAI58418;
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950 G; 1369 T; 0 other;

Sequence 4798 BP; 1629 A; 850 C;

Length: 592 Gaps: 21 Percent Identity: 28.547

506.50 1.549 55.236

Quality:
Ratio:
Percent Similarity:

alignment_scores:

alignment_block: US-09-600-358A-	L_block: 00-358A-4 x AAI58418
Align s	seg 1/1 to: AAI58418 from: 1 to: 4798
2 1682	AspGlnArgGluIleLeuGlnLysg ::: ::: :::::::::: GAACAGCAGGAGCTTGTTGAAAGGGATGATGAAAACAACTGATGAATGT 1731
10	GGAGCCAATCCATGCAGATTTTGTTGAAACTTATAAGAGGAAGATTG 1781
20	hrLysGluGluPheAlaAsnGluPheLeuLysLeuLysArgGln 34 ::
35 1832	SerThrLysTyrLysAlaAspLysThrTyrProThrThrValAlaGluAs 51
51	nalalysasnilelyslysasnargtyrlysaspileleuProfyraspī 68 : ::
68 1914	yrSerargValGluLeuSerLeuIleThrSerAspGluAspSerSerTyr 84 :::
85 1964	IleAsnAlaAsnPheIleLysGlyValTyrGlyProLysAlaTyrIleAl 101
101	aThrGlnGlyProLeuSerThrThrLeuLeuAspPheTrpArgMetIler 118 ::: ::: :::
118 2064	rpGluTyrSerValLeuIleIleValMetAlaCysMetGluTyrGluMet 134 ::::: ::: :: GGGAACAGAAAGCCACAGTTATTGTCATGGTCACTGTGAAGAAGGA 2113
135	GlyLysLysLysCysGluArgTyrTrpalaGluProGlyGluMetGlnLe 151 ::::::: ::: ::: AACAGGAACAAGTGCGGAATACTGGCCGTCATGGAAGGGCACTCG 2163
151 2164	uGlupheGlyProPheSerValSerCysGluAlaGluLysArgLysSerA 168
168 2214	sptyrileileargthrleuLysValLysPheasnSerGlu 181 :::
182	.ThrargThr11eTyrGlnPheHisTyrLysAsnTrpProAspHisAspV 198
198 2314	alProSerSerIleAspProlleLeuGluLeulleTrpAspValArgCys 214 ::::: GCCTGAGGATCCTCAACTGAAAGAGAGAGAGAGAGGATGCC 2363
215 2364	TyrglnGluAspAspSerValProIleCysIleHisCysSerAlaGlyCy 231 :::::::
231	sGlyargThrGlyVallleCysAlaIleValAspTyrThrTrpMetLeuL 248 :: TGGGCGCACAGGAACCTATATCGGAATTGATGCCA 2448
248	euLysAspGlyIleIleProGluAsnPheSerValPheSerLeuIle 263 :: :: :: ::: ::: ::: TGCTAGAAGGCCTGGAAGAACAAAGAGGTTTATGGTTATGTT 2498

2499	ArgGluMetArgThrGlnArgProSerLeuValGlnThrGlnGluGlnTy .::::	280
280	UULeuValTyrAsnalaValLeuGluLeuPheLysA 	
295	AspvalileargasplyshisSerGlyThrGluSerGlnAlaLys 	1 9
312	CyslleProGluLysAsnHisThrLeuGlnAlaAspSerTyrSerProAs	328 2692
328	EMet. : FGGA	344
344	rgThrLysMetGluIleLysGluSerSerSerPheAspPheArgThrSer:::: :: ::: :: :: :: :: :: ::	360 2792
361	GluIleSerAlaLysGluGluLeuValLeuHisPr ::::: ::: ::: AGAGTGCCACTTAAACATGAGCTGGAAATGAGTAAAGAGAGGTGAGCATGA	372
372	oAlaLysSerSerThrSerPheAspPheLeuGluLeuAsnTyrSerPheA::: :: ::: TTCAGATGAATCCTCTGATGATGACAGTGATTCAGAGGAACCAAGTAAT	389 2892
389	splysasnalaaspThrThrMetLysTrpGlnThrLysAlaPhePro	404
405	IleValGlyGluProLeuGlnLysHisGlnSerLeuAspLeuGlySerLe:::	421 2989
421	TTGTT	423
424	GluglyCysSerAsnSer ::: \ACCAGGAAATCTGTGCTCAGTACTGGGGAGAAGGA	432
433	nalaalaGlyargTyrPheAsnSerLysValProlle :::	448 3124
449	hrProPheGluLeuIle :: :: caacttatacccrrcGrgrctt	463
463	rtyr	472 3224
473	GAGCAGCTTCCTGCAGAACCCAAGGATTAATCTCTATGATTCAGGTCGT	486 3274
486 3275	nalaGlnLysValMetHisValSerSerAlaGluLeuAsnTyrSerLeuP ::::::::::: CAAACAAAAGTTCCCCAGAAGAATTCCTCTGAAGGGAAC	503 3314
503	gAsnAlaSerAsnValLysHisHis 	519 3323

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64 LeuProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAspGl
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                                                   seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1994.DAT:AAQ45353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This DNA may be expressed in a prokaryotic or eukaryotic host for the production of a PTP-1D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein tyrosine phosphatase (PTP) protein, PTP-ID - are useful for diagnosis and treatment of diseases associated with abnormal PTP-ID levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         888 ACTACAACAACAGGAGTGCAAACTT.....CTCTACAGCCGAA 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 AlaGlnSerLysLysIleThrLysGluGluPheAlaAsnGluPheLeuLy 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 sLeuLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThrT 47
                                                                                                                                                                                                   Protein-tyrosine-phosphatase; enzyme; disease diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 712 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 441
Gaps: 15
Percent Identity: 31.293
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                                                                                                                                                                        Human protein-tyrosine-phosphatase-1D DNA
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130..1911
/*tag= a
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                        3324 AAGAGTACACCTCTACTCATTCAC 3347
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520 AspSerSerAlaLeuGlyValTyr 527
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                                                                          seq_documentation_block:
ID AAQ45353 standard; DNA; 2790
                                                                                                                                                                                                                                                                                                                                                             93WO-EP02728
                                                                                                                                                                                                                                                                                                                                                                                       92US-0956315
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                                                                                                                                             09-OCT-1994 (first entry)
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Ratio: 1.972
Percent Similarity: 57.143
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US-09-600-358A-4 x AAQ45353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-135583/16.
P-PSDB; AAR52991.
                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             36-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                     06-0CT-1992;
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                                                                                                                                                                                                                                                                                                         WO9408017-A
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1713
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1764 TAAGTATTCTCTAGCGGACCAGACGAGTGGAGATCAGAGCCCTCTCCCGC 1813
                                                                                                                                 1126 TGCCTGCAAAAACACGGTGAATGACTTTTGGCGGGATGGTGTTCCAAGAAA 1175
                                                                                                                                                                                                                                                                                           1226 AATGTGCTCAATACTGG.....CCTGATGAGTATGCTCTAAAAGAATAT 1269
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976 CTGCCCTTTGATCATACCAGGGTTGTCCTCACGATCTGTGATCCCAATGA 1025
                                                     216
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                                                                                                                                                                                                                                                                                                                                                                                                                      GlyProPheSerValSerCysGluAlaGluLysArgLysSerAspTyrIl 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 luLeuValTyrAsnAlaVal.....LeuGluLeuPheLysArgGln 294
                                                                                                                                                                                                                                                                   121 rValLeulleIleValMetAlaCysMetGluTyrGluMetGlyLysLysL 138 :::||||||||||:::
                                                                                                                                                                                                                                                                                                                                                 ysCysGluArgTyrTrpAlaGluProGlyGluMetGlnLeu...GluPhe 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elleArgThrLeuLysVal......LysPheAsnSerGluThrA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 rgThrIleTyrGlnPheHisTyrLysAsnTrpProAspHisAspValPro 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264
                                                                                                                                                                                         ProLeuSerThrThrLeuLeuAspPheTrpArgMetIleTrpGluTyrSe 121
                                                                                                               ...........GlyProLysAlaTyrIleAlaThrGlnGly 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 LeuLysAspGlyIleIleProGluAsnPheSerValPheSerLeuIleAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 ......ValIleArgAspLysHisSerGlyThrGluSerGlnAlaLysH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 SerSerIleAspProIleLeuGluLeuIleTrpAspValArgCysTyrGl
                                     80 uAsp...SerSerTyrIleAsnAlaAsnPheIleLysGlyValTyr....
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496.00
1.824
53.021
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888888888888
                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:AAS92612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) and (II) and (II) and (II) are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                         2013
             1864 GTCTATGAAAACGTGGGCCTGATGCAACAGCAGAAAGTTTCAGATGAGA 1913
                                                                                                                                            SerThrThrLysAlaA
                                                                                                                                                                                          354 SerPheAsp......PheArgThrSerGluIleSerAlaLysGl
                                                                                                                                                                                                                          2014 GGATTTGGAAGGCTTGCAATGTGGTTGACTACCTTTTGATAAGCAAATT
                                                                                                                                                                                                                                                             366 uGluLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuG
                                                                                                                                                                                                                                                                                               2064 TGAAACCATTTAAAGACCACTGTATTTTAACTCAACAATACCTGCTTCCC
                                                                                  1914 AAACCTGCCAAAACTTCAGCACAGAAATAGATGTGGACTTTCACCTCTCC
                                                                                                                   337 laLysMetMetAsnGlnGlnArgThrLysMetGluIleLysGluSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JNA encoding novel human diagnostic protein #28416.
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                                                                                                                                                                                                                                                                                                                                                                      2114 AATTACTCATTTCCTCAGATAAG 2136
                                                                                                                                                                                                                                                                                                                                    383 luLeuAsnTyrSerPheAspLys 390
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ID AAS92612 standard; cDNA; 4823
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2000US-0649167
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disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3190 GTGACTTCAAAGTAACGTGTGTAGAAATGGAACCACTTGCTGAATATGTA 3239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......GATGTAGCTAAAAAAGATCAAA 2898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 lyProLeuSerThrThrLeuLeuAspPheTrpArgMetIleTrpGluTyr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 AspSerValProIleCysIleHisCysSerAlaGlyCysGlyArgThrGl 235
                                                                                                                                                                                                                                                                                                                                                          Sequence 4823 BP; 1388 A; 1075 C; 1117 G; 1243 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3240 GTTAGGACATTCACCCTGGAAAGGAGGGGGTACAATGAAATCCGTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3290 TAAACAGTTCCATTTCACGGGCTGGCCTGACCATGGAGTGCCCTACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LysGluGluPheAlaAsnGluPheLeuLysLeuLysArgGlnSerThrLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2899 ATAGAGCAAAAACCGATATGGAAACATTATAGCATATGATCACTCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snIleLysLysAsnArgTyrLysAspIleLeuProTyrAspTyrSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aAsnPheIleLysGlyValTyrGlyProLysAlaTyrIleAlaThrGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3049 GTCCCGTTCATGAAACAGTGTATGATTTCTGGAGGATGATTTGGCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SerValLeuIleIleValMetAlaCysMetGluTyrGluMetGlyLysLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 sLysCysGluArgTyrTrpAlaGluProGlyGluMetGlnLeuGluPheG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 IleArg.....ThrLeuLysValLysPheAsnSerGluThrArgThrIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 sTyrLysAlaAspLysThrTyrProThrThrValAlaGluAsnAlaLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eTyrGlnPheHisTyrLysAsnTrpProAspHisAspValProSerSerI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 513
Gaps: 18
Percent Identity: 28.460
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4233 ATACTTCAGGTGGAAAAGTGGCAGGAGGAATGCAAGGAG 4271

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3390 AGTGCTGGCCCCATCGTTGTACATTGCAGTGCTGGTGCTGGACGAACTGG 3439
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.....arcgrcacaataccctctgccaacactgtaaaa 3938
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3939 GACTTCTGGAGATTAGTGTATGATTATGGCTGTACCTCCATTGTGATGTT 3988
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4089 GACTGTGATGATCAACCGGATTTTTAGGATATGCAATCTAACAAGACC 4138
                                                                                                                                                        3440 CIGCTACATIGIGALIGACATCAIGCTAGACAIGGCIGAAAGAGAGGGGIG 3489
                                                                                                                                                                                                                                                                                         3490 TIGIT......GATATTTACAATTGTGTCAAAGCCTTAAGATCT 3527
                                                                                                                                                                                                                                                                                                                                                                                         ||||||||
3628 aatttaaagctgcatattttgatatgattagaatagactcccagactaac 3677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3728 ACTACAAGCTGAAGACTGCAGTATAGCGTGCCTGCCA...AGGAACCATG 3774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3825 TTAATTACAATTGATGGGGAGAGCAGTAACTACATCAATGCTGCTCTTAT 3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3989 AAACGAAGTCGACTTGTCCCAGGGCTGCCCTCAGTACTGGCCAGAGGAAG 4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4139 ACAGGAAGGTTATCTGATGGTGCAACAGTTTCAGTACCTAGGATGGGCTT 4188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3678 TCTTCACATCTCAAGGATGAATTTCAGACTCTGAATTCAGTCACCCCTCG 3727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3775 ACAAGAACCGTTTCATGGACATGCTGCCACCTGACAGATGTCTGCCTTTT 3824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 heAsnSerLysValProlleThrArgThrLysSerThrProPheGluLeu 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 erAlaLysGluGluLeuValLeuHisProAlaLysSerSerThrSerPhe 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .......AspLysAsnAlaAspThrThrMetLysTrpGlnThrLysA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 laPhe.....ProlleValGlyGluProLeuGlnLySHisGln 414
                                                                                                                                                                                                                      252 leIleProGluAsnPheSerValPheSerLeuIleArgGluMetArgThr 268
                                                                                                                                                                                                                                                                                                                                                    269 GlnArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValTyrAs 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 SerThrThrLysAlaAlaLysMetMetAsnGlnGlnArgThrLysMet.. 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 .... GlulleLysGluSerSerSerPheAspPheArgThrSerGlulleS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3875 GGACAGCTACAGCCACCAGCTGCTTTC.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 ......CyslleProGluLysAsnHisT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 hrLeuGln.....AlaAspSerTyrSerProAsn.....LeuProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 AspPheLeuGluLeuAsnTyrSerPhe...........
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                                                                                            235 yValIleCysAlaIleValAspTyrThrTrpMetLeuLeuLysAspGlyI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AspLysHisSerGlyThrGluSerGlnAlaLysHis......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 ..PheLys...ArgGlnMetAspVallleArg.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 nAlaValLeuGluLeu......
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seq_name: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AA208539 The present sequence encodes human protein phosphatase k (HPTPK). Human protein phosphatase, base sequence thereof and amino acid sequence thereof NoAbstract 2721 TTGG.....GATGTAGCTAAAAAGATCAAA 2746 Sequence 5775 BP; 1711 A; 1197 C; 1261 G; 1606 T; 0 other; 54 21 LysGluGluPheAlaAsnGluPheLeuLysLeuLysArgGlnSerThrLy 37 37 sTyrLysAlaAspLysThrTyrProThrThrValAlaGluAsnAlaLysA 54 snlleLysLysAsnArgTyrLysAspIleLeuProTyrAspTyrSerArg Length: 513 Gaps: 18 Percent Identity: 28.460 <u>.</u> /product= "protein phosphatase to: 5775 Human protein phosphatase k encoding cDNA. (KOAD) KOREA ADV INST SCI & TECHNOLOGY. Human; protein phosphatase k; HPTPK; ds Location/Qualifiers 16..1438 /*tag= a Disclosure; Page 6-9; 14pp; Korean from: 1 BP. Yang seq_documentation_block:
ID AAZ08539 standard; cDNA; 5775 96KR-0044614 96KR-0044614 MC, (first entry) 496.00 1.824 53.021 Align seg 1/1 to: AA208539 alignment_block: US-09-600-358A-4 x AAZ08539 Byun GH, Hah HJ, Kil WPI; 1999-335582/28. P-PSDB; AAY29591. Quality: Ratio: Percent Similarity: KR98026246-A. 08-OCT-1996; Homo sapiens 08-OCT-1996; alignment_scores: 14-0CT-1999 15-JUL-1998 AAZ08539;

87 aAS 2847 CAA	aAsnPhelleLysGlyvalTyrGlyProLysalaTyrIlealaThrGlnG :: CAACTATATTGATGGCTACCAGAGACCAAGTCATTACATTGCAAG	104 2896
104 lyP 2897 GTC	1yProLeuSerThrThrLeuLeuAspPheTrpArgMet11eTrpGluTyr ::: ::: GTCCGGTTCATGAACAGTGTATGATTTCTGGAGGATGATTTGGCAAGAA	120 2946
121 Ser ::: 2947 CAA	erValLeullelleValMetalaCysMetGluTýrGluMetGlyLysLy aatctGCTTGCATGTGATGGTTACAAATTTAGTTGAGGTTGGCCGGGT	137 2996
137 SLY. 2997 TAA	SLySCysGluArgTyrTrpAlaGluProGlyGluMetGlnLeuGluPheG ::: ::: TAAATGCTATAAATATTGGCCTGATGATACTGAAGTTTATG	154 3037
154 lyP 3038 GTG	1yProPheSerValSerCysGluAlaGluLysArgLysSerAspTyrIle ::: ::: GTGACTTCAAAGTAACGTGTGTAGAAATGGAACCACTTGCTGAATATGTA	170 3087
171 Ile ::: 3088 GTT	lleargThrLeuLysValLysPheAsnSerGluThrArgThrIl ::: :: :: :: :: GTTAGGACATTCACCCTGGAAAGGAGGGGGTACAATGAAATCCGTGAAGT	185 3137
185 eTy. : 3138 TAA	eTyrGlnPheHisTyrLysAsnTrpProAspHisAspValProSerSerI : TAAACAGTTCCATTTCACGGGTGGCCTGACCATGGAGTGCCCTACCATG	202 3187
202 leA	leaspprolleLeuGluLeulleTrpaspValargCysTyrGlnGluasp 	218 3237
219 Asp. ::: 3238 AGT	AspSerValProIleCysIleHisCysSerAlaGlyCysGlyArgThrGl ::::: :::	235 3287
235 yva. 3288 CTG	yVallleCysAlalleValAspTyrThrTrpMetLeuLeuLySAspGlyI 	252 3337
252 lelle ::::: 3338 TTGTT	IleProGluAsnPheSerValPheSerLeulleArgGluMetArgThr 	268 3375
269 Gln3 ::: 3376 CGG	GINArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValTyrAs ::: ::::: :: CGGCGTATTAATATGGTCCAGACAGAGGAACAGTACATTTTATTCATGA	285 3425
285 nAla :11 3426 TGC	nAlaValLeuGluLeu	290 3475
291P	PhelysArgGlnMetAspVallleArg	299 3525
300 Asp	PLYSHISSErGlyThrGluSerGlnalaLySHis	311 3575
312	TACAAGCTGAAGACTGCAGTATAGCGTGCCTGCCAAGGAACCATG	319 3622
319 hrLd 3623 ACA	LeuGlnLeuProLys :::	331 3672
332 S	ThrLysAlaAlaLysMetMetAsnGlnGlnArgThrLysMet	7
36/3 TTA		3722 363

3723	3723 GGACAGCTACAGGCAACCAGCTGCTTTC	3750
363	erAlaLysGluGluLeuValLeuHisProAlaLysSerSerThrSerPhe	379
3751	751ATGGTCACACAATACCCTCTGCCAAACATGTAAAA 3786	3786
380		388
3787		3836
389	AspLysAsnAlaAspThrThrMetLysTrpGlnThrLysA	402
3837	3837 AAACGAAGTCGACTTGTCCCAGGGCTGCCCTCAGTACTGGCCAGAGGAAG 3886	3886
402	laPheProlleValGlyGluProLeuGlnLySHiSGln 414	414
3887		3936
415	SerLeuAspLeuGlySerLeuLeuPheGluGlyCysSerAsnSerLysPr	431
3937	GACTGTGATGTGATCAACCGGATTTTTAGGATATGCAATCTAACAAGACC	3986
431	oValasnalaalaGlyArgTyrP 43	439
3987	3987 ACAGGAAGGTTATCTGATGGTGCAACAGTTTCAGTACCTAGGATGGGCTT 4036	4036
439	heAsnSerLysValProlleThrArgThrLysSerThrProPheGluLeu	455
4037	CTCATCGAGAAGTGCCTGGATCCAAAAGGTCATTCTTGAAACTG	4080
456	IleGlnGlnArgGluThrLysGluValAspSerLysGlu 468	
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51 ASNAIALYSASNIIELYSLYSASNARGTYTLYSASPIIELEUPROFYRAS
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Quality: 3615.00
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LOCUS AX020263
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gb_ro:RNLCaR
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                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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VERSION
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Mouse 200 kD T-cell leu
Mouse Ly-5 (leucocyte-c
Sequence 118 from Paten
                                                                                                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Y00065 Rat mRNA for leucocy
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AY026862 Mus musculus brain
AY026661 Mus musculus brain
AF162856 Mus musculus recep
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammanlai; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2356)
Roifman,C.M.
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Patent: WO 9936548 + 3 22-JUL-1999;
HSC RES DEV LP (CA); ROIFMAN CHAIM M (CA)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2356)
Cohen, S., Dadi, H., Shaoul, E., Sharfe, N. and Roifman, C.M.
Cloning and characterization of a lymphoid-specific, inducible human protein tyrosine phosphatase, Lyp
Blood 93 (6), 2013-2024 (1999)
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/note="splice variant of lymphoid phosphatase LyPl"
/codon_start=1
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Homo sapiens lymphoid phosphatase LyP2 mRNA, complete cds.
AF001847
                              2042 TGACTCTGTGATACTTAGACCAAGCAAGAGTGTAAAACTCCGAAGTCTA 2091
pAspSerVallleLeuArgProSerLysSerValLysLeuArgSerProL 684
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/db_xref="taxon:9606"
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92 GAAAATTACTAAAGAGGAGTTTGCCAATGAATTTCTGAAAGCTGAAAAGGC 141
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                                                                                         51 AsnAlaLysAsnIleLysLysAsnArgTyrLysAspIleLeuProTyrAs
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Patent: WO 9936548-A 1 22-JUL-1999;
HSC RES DEV LP (CA); ROIFWAN CHAIM M (CA)
Location/Qualifiers
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/note="unnamed protein product"
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Sequence 1 from Patent W09936548.
AX020261
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Mammalia; Eutheria; Pri
1 (bases I to 3058)
Roifman, C.M.
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to: 3058

from: 1

Align seg 1/1 to: AX020261

Page 5

AspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17	SILEThrlysGluGluPhealaAsnGluPheLeuLysLeuLysArgG 34	erThrLysTyrLysAlaAspLysThrTyrProThrThrValAlaGlu 50	AlaLysasnileLysLysAsnargTyrLysAspIleLeuProTyras 67	rSerargValGluLeuSerLeulleThrSeraspGluAspSerSerr 84	leasnalaasnPheileiysGlyValTyrGlyProLysalaTyrile 100	ThrGlnGlyProLeuSerThrThrLeuLeuAspPheTrpArgMet11 117	PGlutyrServalLeuileilevalMetalacysMetGlutyrGluM 13	JyLysLysLysCysGludrgTyrTrpAlaGluProGlyGluMetGln 150	GlupheGlyPropheSerValSerCysGlualaGluLysargLysSe 167	PTyrileileargThrLeuLysValLysPheasnSerGluThrargT 184		IleaspproileLeuGluLeuIleTrpaspValargCysTyrGlnG 217	pAspSerValProIleCysIleHisCysSerAlaGlyCysGlyArgT 234	1yvalilecysalailevalaspTyrThrTrpMetLeuLeuLysasp 250	lleileprogluðsnPheSerValPheSerLeulleargglumetar 267	rGlnargProSerLeuValGlnThrGlnGluGlnTyrGluLeuValT 284	nAlavalLeuGluLeuPheLysargGlnMetAspVal
1 Metas 42 ATGGA	17 sLysI 92 GAAAA	34 InSer 142 AATCT	- C	Si — A	0 - ()	101 AlaTh 342 GCCAC	(2) (2)	134 etGly 42 TGGGA	151 LeuGl 492 CTGGA	167 rAspT 542 TGATT	184 hrile 592 CTATC	201 Seril 642 TCTAT	217 uAspAa 692 GGATG	234 hrGly 742 CTGGT	251 GlyIl 792 GGGAT	267 gThrG 842 GACAC	284 yrAsni 892 ACAATC

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EAEKRKSDYIIRTLKVKFNSETRITYQFHYKNWPDHDVPSSIDPILELLWDVRCYQED
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1 (bases 1 to 3058)

Cohen, S., Dadi, H., Shaoul, E., Sharfe, N. and Roifman, C.M.
Cloning and characterization of a lymphoid-specific, inducible human protein tyrosine phosphatase, Lyp
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Submitted (30-APR-1997) Immunology and Allergy, The Hospital For
Sick Children, 555 University Avenue, Toronto, Ontario M5G 1X8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AF001846 3058 bp mRNA linear PRI 01
DEFINITION Homo sapiens lymphoid phosphatase LyP1 mRNA, complete cds.
VERSION AF001846. GI:4100631
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Rolfman, C.M.
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                                                                                                                                                                                                                                                                                                              AlaThrGlnGlyProLeuSerThrThrLeuLeuAspPheTrpArgMetIl
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us-09-600-358a-4.rge

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Unknown.

Unclassified.

Unclassified.

NCE 1 (bases 1 to 3580)

ORS Jallal, B. and Plowman, G. D.

Diagnosis and treatment of PTP04 related disorders and treatment of PTP04 related disorders.

Location/Qualifiers

Location/Qualifiers

1. 3580

1. 3580

1. 3580

1. 3580
1992 ATTGGAACATCACTGGAATGGGGTGGAACATCTGAACCAAGAAATTTGA 2041
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                                                                                         erLeuSerLeuAsnSerProThrAsnIleSerSerLeuLeuAsnGlnGlu
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Percent Identity: 99.416
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LOCUS
AR149916
DEFINITION Sequence 1 from patent US 6228641.
VERSION AR149916.1 GI:15114507
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ORIGIN
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ORGANISM
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                          1842
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2000

684

651

634

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FSYYVANTANTSTRIEDGESAVLATAPRIDDEIPLHFLXGTPESSTSL
FSYYVANTANTANTANTANTANTAPRIDDEIPLHFLXGTPESSTSL
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S Huang,C., Zhang,C., Wu,T., Peng,Y., Gu,Y., Zhang,L., Jiang,C.,
Li,Y., Han,Z., Wang,Y., Chen,Z. and Fu,G.
Direct Submission

L Submitted (12-MAY-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai, 201203, P. R. China
Location/Qualifiers

I. 2877

//organism="Homo sapiens"
//db_xref="taxon:9606"
//tissue_type="adrenal gland"
                                                                                                                                                                                                                                                                                                                                                                                                                       AF150732 2877 bp mRNA linear PRI 04-MAY-2000
Homo sapiens protein tyrosine phosphatase (PTP) mRNA, complete cds.
AF150732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 2877)
Huang.C., Zhang.C., Wu.T., Peng.Y., Gu.Y., Zhang.L., Jiang.C.
Li.Y., Han.Z., Wang.Y., Chen.Z. and Fu.G.
A novel gene expressed in human adrenal gland
                                      luPheSerProAsnValProLysSerLeuSerSerAlaValLysValLys
                                                                                                    IleGlyThrSerLeuGluTrpGlyGlyThrSerGluProLysLysPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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AUTHORS
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JOURNAL
REFERENCE
                                                         1950
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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                               71 ATGGACCAAAGAGAATTCTGCAGAAGTTCCTGGATGAGGCCCAAAGCAA
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Percent Identity: 89.229
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267

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334	hrLysAlaalaLysMetWetAsnGlnGlnArgThrLysWetGluIleLys 350 	
351 1118	GluSerSerPheAspPheArgThrSerGluIleSerAlaLysGluGl 367 	
367 1168	uLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuGluL 384 :::	
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434	AlaAlaGlyArgTyrPheAsnSerLysValProIleThrArgThrLysSe 450 	
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534	GluasnProTyrPheserSerTrpProProSerGlyThrSerSerLysMe 550 	
550	tSerLeuAspLeuProGluLysGlnAspGlyThrValPheProSerSerL 567 	

MUSPROTYPH 2734 bp mRNA linear ROD 27-APR-1993 Mouse protein tyrosine phosphatase (70zpep) mRNA, complete cds. M90388 M90388 1 G1:200522 M90388 Protein-tyrosine phosphatase. Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2734)
Matthews, R.J., Bowne, D.B., Flores, E. and Thomas, M.L.
characerization of hematopoletic intracellular protein tyrosine
phosphatases: Description of a phosphatase containing an SH2 domain
and another eriched in proline-, glutamic acid-, serine-, and
threonine-rich sequences /Translation-"MOOREILOQULKEAQKKKINSEEFASEFIKKKROSTKYKADKIY
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KSTPFELJOORKTNDLAVGDGFSCLESQLHEHYSLRELQVQRVAHVSSEELNYSLPGA
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           uAspAspSerValProlleCysIleHisCysSerAlaGlyCysGlyArgT
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as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                    Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 RP5-107303 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the entire insert of clone RP5-107303 The true right end of clone RP11-215C20 is at 30467 in this sequence. The true right end of clone RP11-324J2 is at 119169 in this sequence. Location/Qualifiers
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/note="Alusx repeat: matches 1. .298 of consensus"

9793. .10559

/note="LiMC1 repeat: matches 5526. .6320 of consensus"

10574. .10730

/note="MIR repeat: matches 95. .262 of consensus"

10759. .10907

/note="MIR repeat: matches 2. .139 of consensus"

10908. .11219
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7.0016="L2 repeat: matches 2655. .2705 of consensus" 2305. .2446
7.0016="MIR repeat: matches 40. .176 of consensus" 5652. .5913. 7.0016="MIR repeat: matches 5524. .5813 of consensus" 6295. .6428
7.0016="MIR repeat: matches 5524. .5813 of consensus" 6695. .6428
6653. .6700
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/1016. .13149
/note="MER58B repeat: matches 70. .341 of consensus"
13150. .13435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-5"
257. .322
/note="MER5A repeat: matches 41. .109 of consensus"
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/note="AluSx repeat: matches 1. .312 of consensus"
1348. .1698
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/note="8 copies 6 mer acacac 97% conserved"
7925. .7980
/note="28 copies 2 mer aa 75% conserved"
8071. .8369
/note="Alusx repeat: matches 1. .296 of consensus"
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11220. .11315
hote="MIR repeat: matches 139. .237 of consensus"
12210. .12464
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3458. .13805
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                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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14431. .14563
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/clone="RP5-107303"
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14118. .14430
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On Jul 19, 2001 this sequence version replaced gi:14566004.

During sequence assembly date as compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission only a small overlapping clone, as we submit sequences with an all overlapping clone, as we submit sequences with residence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL137856 143618 bp DNA linear PRI 17-JUL-2001
Human DNA sequence from clone RP5-107303 on chromosome lpl3.1-13.3,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (17-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2039 CTGGTGGTAACATTTGGAGCATCACCAGAATGCAGTGGGACATCTGAAAT 2088
        snSerHisSerSerLeuSerLeuAsnSerProThrAsnIleSerSerLeu 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 ulleProProLeuProValArgThrProGluSerPhelleValValG 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1995 AGGAAGCCGGAGAGCCCTCACCAGGTGTTACCGAATCCTTA.....CCT
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                                                                                                                                                                                                                                                                                                     563 eProSerSerLeuLeuProThrSerSerThrSerLeuPheSerTyrTyrA
                                                                                   530 leProLeuValGluAsnProTyrPheSerSerTrpProProSerGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAsnGlnGluSerAlaValLeuAlaThrAlaProArgIleAspAspGl
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1 (bases 1 to 143618)
Glithero, R.
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14565 /note="A	14861. /note="	1491015 /note="L1M	15230. /note="1	/note="	/note	16840 /note	on 1/4/2 /note	e 1883919765 /note="CpG isl	/evidence=not_experimental gion 2038520649	/note="A	/note="F gion 22760	/note="A	/note="A	/note="L gion 23590	/note="1	/note="A	/note="A	/note="	/note="?	/note="M	/note="(/note=	/note=	/note="	/note='	/note="	/note="	/note=",	/note="	/note="1	/note="1	/note="9	/note="A	/note=	33/4/ /note="A
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/note="L1ME repeat: matches 5644. .5823 of consensus"

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34786. .34930
/note="FLAM C repeat: matches 12. .142 of consensus"
34931. .35225
/note="Lime repeat: matches 5265. .5563 of consensus"
35257. .35727
/note="Lime repeat: matches 4762. .5233 of consensus"
35743. .36021
/note="AluJD repeat: matches 1. .287 of consensus"
36340. .36488
/note="Line repeat: matches 6009. .6157 of consensus"
3739. .37776
/note="Line repeat: matches 6009. .6157 of consensus"
37329. .37776
/note="Line repeat: matches 7275. .7680 of consensus"
38067. .38121
                                                                                                                                                                                                                                                                                                                                               /note="AluSc repeat: matches 1. .294 of consensus"
39575. .39657
/note="AluSc/FRAM repeat: matches 206. .289 of consensus"
4.1057
/note="AluJo repeat: matches 5. .293 of consensus"
/note="AluJo repeat: matches 5. .293 of consensus"
/note="AluJv repeat: matches 1. .311 of consensus"
4.3028. 4.3036
                                                                                                                                                                                                                                      #5710 AAGAGTCAAGCAAAGCATTGTATTCCTGAGAAAAATCACACTCTCCAAGC 45661
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Gaps: 2
Percent Identity: 86.087
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US-09-600-358A-4 x AL137856/rev
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Ratio: 4.985
ilarity: 86.667
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Human mRNA for protein-tyrosine-phosphatase G1, complete cds.
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1 (bases 1 to 2938)
Takekawa,M., Itoh,F., Hinoda,Y., Arimura,Y., Toyota,M., Sekiya,M., Adachi,M., Imai,K. and Yachi,A.
Cloning and Characterization of a human cDNA encoding a novel putative cytoplasmic protein-tyrosine-phosphatase
Blochem. Biophys. Res. Commun. 189 (2), 1223-1230 (1992)
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Homo sapiens adult colon cDNA to mRNA, clone_lib:Clontech
                                   543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544 SerGlyThrSerSerLysMetSerLeuAspLeuProGluLysGlnAspGl 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 erTyrTyrAsnSerHisSerSerLeuSerLeuAsnSerProThrAsnIle 593
410 uGlnLysHisGlnSerLeuAspLeuGlySerLeuLeuPheGluGlyCysS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 eArgAsnAlaSerAsnValLysHisHisAspSerSerAlaLeuGlyValT
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Takekawa, M.
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D13380.1 GI:220033
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/ULSBUE_TYPE - CANDING SOURCE |
//LISBUE_TYPE - CANDING SOURCE |
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//Product="Protein tyrosine phosphatase G1" |
//Product="Protein tyrosine phosphatase G1" |
//Drotein_16="BAA02648.1" |
//DROTEIN_TRANSFOLLERPENSERVETERPENSERVERFERVERFERVERFER STRYPTICATE STRYPTI
University, Internal Medicine (Section1); South 1, West Chuo-ku, Sapporo 060, Japan (E-mail:Kimura%sapmed.ac.jp@vax2.nlm.nth.gov, Tel:011-611-2111(ex.3211), Fax:011-613-1141) Submitted (09-OCT-1992) to DDBJ by: Mutsuhiro Takekawa Dept. of Internal Medicine Section I Sapporo Medical College South 1, West 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1) GAAGAGTCCTGACCACAATGGGGAGGACAACTTCGCCCGGGACTTCATGC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 783
Gaps: 25
Percent Identity: 37.037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism~"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref~"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        011-611-2111 x3211
011-613-1141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1157.00
Ratio: 2.400
Percent Similarity: 61.558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: HUMPTPG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-600-358A-4 x HUMPTPG1
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355	352 SerSerP 090 GGAACTCATCCAGCGACCATGTGACCTTCTCCCCTTCAGCTT	Н
0	::: ::: ::: 46TGCCTTGTTGAAGGGATGCTAAAGAAAAAAAAATACTGCAGCCAC	7
51	laLysMetMetAsnGlnGlnArgThrLysMetGluIleLysGlu	
336	320 euGlnAlaAspSerTyrSerProAsnLeuDroLysSerThrThrLysAla	
320	303 rGlyThrGluSerGlnAlaLysHisCyslleProGluLysAsnHisThrL ::: :::::::::::::::::::::::::::	
303	297 ValLysHisse ::: :::::::::::::::::::::::::::::::	
296 916		
280	263 eArgGluMetArgThrGlnArgProSerLeuValGlnThrGlnGluGlnT ::::	
263 816	247 LeuLeuLysAspGlyIleIleProGluAsnPheSerValPheSerLeuIl 	
246	230 lycysGlyArgThrGlyValileCysAlaIleValAspTyrThrTrpMet 	
230	213 gcystyrGlnGluAspAspSerValProlleCys1leHisCysSerAlaG 	
213 669	197 AspValProSerSerIleAspProIleLeuGluLeulleTrpAspValAr 	
196 619	180 erGluThrargThrIleTyrGlnPheHisTyrLysAsnTrpProAspHis :: :: :::	
180	163 uLysArgLysSerAspTyrIleIleArgThrLeuLysValLysPheAsnS ::: :::: :::	
163 519	147 GlyGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGl 	
146 469	130 etGluTyrGluMetGlyLysLysCysGluArgTyrTrpalaGluPro :::	
130	113 eTrpArgMet11eTrpGluTyrSerValLeu11eI1eValMetAlaCysM 	
113 369	97 LysalatyrilealathrGlnGlyProLeuSerThrThrLeuLeuAspPh 	
96 319	80 luAspSerSerTyrIIEAAnAlaAsnPheIIeLysG1yValTyrG1yPro :: :::	

1140		1189
369	ValLeuHisProAlaLysSerSerThrSerPheAspPheLeuGluLe	384
38		387
1240	CAGAACTTCCAGGGAAAAATGAATCAACAATTG	1289
388 1290	PheaspLysasnalaaspThrThrMetLysTrpGlnThrLysala 4	402 1339
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419	TTAAAATTAAATCTGCTTCACCTT	426 1427
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434	AlaalaGlyArgTyrPheAsnSerLysValProIleThrArgThrLysSe (:::::	450 1527
450	r	462 1577
462	ysGluvalAspSerLysGluAsnPheSerTyr 4 ::: ::: ::::::::::::::::::::::::	472 1627
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489	ASDTYT	500
501	serLeuProTyrAspSerLysHisGlnIleArgAsnAlaSerAsnVal :	516 1765
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533	rpProProSerGlyThrSerSerLysM ::: :: arccactrcactcrGarGaCrCa	550 1837
550 1838	etSerLeuAspLeuProGluLysGlnAspGlyThrValPheProSer 5	565 1879
566	SerLeuLeuProThrSerSerThrSerLeuPheSerTyrTyrAsnSerHi : :: :: :: :: :: :: : : : : :	582 1929
582 1930	sSerSerLeuSerLeuAsnSerProThrAsn11eSerSerLeuLeuAsnG ::: ::: ::: ::: TGAAAGCATTTCTACTAGGAAAGTATTGCCAATGTCCATTGCTAGACATA]	599 1979
599	InGluSerAlaValLeuAlaThrAlaProArgIleAsp 6	611

```
This STS was developed from sequence determined by another investigator. See GenBank record: D13380 For additional information about the NHGRI chromosome 7 mapping project, see http://www.nhgri.nlh.gov/DIR/GTB/CHR7. Also see Genomics 11:548-64 (1991) [MUID-92128937].
Location/Qualifiers
1. .2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 LysalaTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAspPh 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 eTrpArgMetIleTrpGluTyrSerValLeuIleIleValMetAlaCysM 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 etGluTyrGluMetGlyLysLysLysCysGluArgTyrTrpAlaGluPro 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 sLyslleThr.....LysGluGluPheAlaAsnGluPheLeuL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 ATGGAGCAAGTGGAGATCCTGAGGAAATTCATCCAGAGGGTCCAGGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 1157.00 Length: 783
Ratio: 2.400 Gaps: 25
Percent Similarity: 61.558 Percent Identity: 37.037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 t
                                                                                                                                                                                                                                                                                                                               /clone_lib="Eric D. Green"
                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2815. .2832)
                                  1.5 mM
100 mM
10 mM
5 mM
8.6
                                                                                                                                                                                                                                                                                                                                                                  /gene="PTPN12"
2760. .2832
/gene="PTPN12"
2760. .2778
/gene="PTPN12"
                                                                    Tris-HCl:
NH4Cl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: G18337
                                      MgC12:
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US-09-600-358A-4 x G18337
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                     Buffer:
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BASE COUNT 10
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                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                         STS
                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STS 28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Members 1 to 2938)

Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F.,
Weintraub.L.A., Mohr-Tidwell, R.M., Peluso, D.C., Fulton, R.S.,
Leckie, M. P. and Green, E.D.

A collection of 1814, human chromosome 7-specific STSs

Genome Res. 7 (1), 59-64 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWSS1985 Eric D. Green Homo sapiens STS genomic, sequence tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 301402201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c 2.50 minute(s)
0.50 minute(s)
0.75 minute(s)
0.75 minute(s)
                                1980 ATATAGCAGGAACAACACATTCAGGTGCTGAAAAAAGATGTTGATGTTAGT 2029
                                                                                                                                                                                                                      2102 ......GTAAGATCGGAATGGAGTGAACTTCAA 2128
                                                                                                                                                                                                                                                                                         2129 AGTCAGGAACGATCTGAACAAAAAGTCTGAAGGC.....TTGAT 2169
                                                                                                         628 lValGluGluAlaGlyGluPheSerProAsnValProLysSerLeuSerS 645
                                                                                                                                                                                                                                                         659 .....GlyThrSerGluProLysLysPheAspAspSerValIleLeuAr 673
                                                                                                                                                                                                                                                                                                                                                      2170 AACCTCTGAAAATGAGAAATGTGATCATCCAGGGGGGGGTATTCACTAT 2218
                                                                                                                                                                                                                                                                                                                                 673 gProSerLysSerValLysLeuArgSerProLysSerGlyLysAsnPhe 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                             2080 AGCAAGTGAA......CATAATACACCT.....
                                                                                                                                                                                645 erAlaValLysValLysIleGlyThrSerLeuGluTrpGly......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 degrees C for 094 degrees C for 095 degrees C for 0972 degrees C for 0973
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each 2 um
each 100 um
0.05 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2938 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human chromosome 7 STSs (1997)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: egreen@nhgri.nih.gov
Primer A: GTAAGAAATTCTGGCATGG
Primer B: TTTTCTAAAACTCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synonyms: PTPN12
GDB: GDB:3754375
GDB_DSEG: PTPN12
Contact: Eric D. Green
Genome Technology Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR Cycles:
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annealing:
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 2938)
Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G18337
G18337.1 GI:1222794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  remplate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Presoak:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STS size: 73
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_sts:G18337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protocol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
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JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
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163 520	ubysarglysSeraspTyrIleIleargThrLeubysValLysPheasnS ::: ::::	180 569	
180 570	erGluThrargThrIleTyrGlnPheHisTyrLysAsnTrpProAspHis:: :::	196 619	
197 620	AspValProSerSerIleAspProIleLeuGluLeuIleTrpAspValAr 	213 669	
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280 867	yrGluLeuValTyrAsnalaValLeuGluLeuPheLysArgGlnMetAsp argaaCtTgTtCataGaGCTATTGCCCAaCTGTTTGAAAAACAGCTACAA	296 916	
297 917	ValLysHisSe ::: CTATATGAAATTCATGGAGAGAATTCCATGAAAATTGCTCATGAAATTGCTCATGGAGTGAAATTGCTCATGGAGTGAAATTGCTCATGAAATTGCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTGCTCATGAAATTATGAAATTGCTCATGAATTGCTCATGAAATGAAATGCTCATGAAATTGCTCATGAAATGAATG	303 966	
303	rGlyThrGluSerGlnAlaLysHisCysIleProGluLysAsnHisThrL::: :: 	320 1009	
320	euGlnalaAspSerTyrSerProAsnLeuProLysSerThrThrLysAla	336 1045	
337	AlaLysMetMetAsnGlnGlnargThrLysMetGluIleLysGlu :: :: :: :: :: :: :: ::	351 1089	
352	GGAACCTCATCCAGTGCCACCCATCTTGACACTTCTCCCCCTTCAGCTT	355 1139	
355 140	heAspPheArgThrSerGluIleSerAlaLysGluGluLeu	368	
369 190	ValLeuHisProAlaLysSerSerThrSerPheAspPheLeuGluLe ::::: ::: CCAGTGTTGCATATGATTCATCAGAACAACATCAGCAGACCTCAACAG	384 1239	
384	UASNITYISEIaaanaanaanaanaanaanaaaaaaaaaaaaaa	387	
388		402	

1290	AACAGATAGATAAAAATTGGAACGAAATTTAAGTTTTGAGATTAAGAAG	1339
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1528	AAACAAAGTTTCAGTTACTCCACCAGAAGAATCCCAGAATTCAGACACAC	1577
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501		516
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2030	:CTCCCCTACCTGAAGAACTCCTGAATCGTTTGTGTT	2079
62	GlyGluPheSerProAsnValProLysSerLeuSerS	1 0
XX	CATAATACACCT	⊣
645	:	658
2102		2128

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30 ysLeuLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThr
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KITAINS 18 1101 - "MEDVELIRKETORVOAMKSPDHNGEDNEARDEMRILRRLSTKYRT
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                                                                                                                                                                                                                                               Human protein tyrosine phosphatase (PTP-PEST) mRNA, complete cds. M93425
M93425 GI:292408
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 3160)

Yang, O.C., Tonks N.N. and Sommercorn, J.
Cloning and expression of PTP-PEST: a novel, nontransmembrane J. Biol. Chem. 268, 6622-6628 (1993)
                                                                   .....TTGAT 2169
                                                                                                                                               2170 AACCTCTGAAAATGAGAAATGTGATCATCCAGCGGGAGGTATTCACTAT 2218
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                                                                                                                gProSerLysSerValLysLeuArgSerProLysSerGlyLysAsnPhe 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 sLysIleThr.....LysGluGluPheAlaAsnGluPheLeuL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIFSDKREQISENPIEAIDIGFGNRCGKPKGPRDPPSEWT
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Gaps: 25
Percent Identity: 37.165
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1. 3160
7. Organism="Homo sapiens"
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30. 2372
                                                                2129 AGTCAGGAACGATCTGAACAAAAAAGTCTGAAGGC
                                                                                                                                                                                                                                                                                                                                                                     protein tyrosine phosphatase.
Homo sapiens cDNA to mRNA.
Homo sapiens
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US-09-600-358A-4 x HUMPTPPEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586
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Ratio: 2.405
Milarity: 61.430
                                                                                                                                                                                                         seq_name: gb_pr:HUMPTPPEST
                                                                                                                                                                                                                                                         seq_documentation_block:
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977 TAACACTGAAAACATGATCAGCTCCATAGAGCCTGAAAAACAA..... 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uLysArgLysSerAspTyrIleIleArgThrLeuLysValLysPheAsnS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 rGlyThrGluSerGlnAlaLysHisCysIleProGluLysAsnHisThrL 320
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                                                                                                                                                                                                                                                                                                                          430 GAGAATTIGAGATGGGAAGGAAAAATGTGAGCGCTATTGGCCTTTGTAT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 erGluThrArgThrIleTyrGlnPheHisTyrLysAsnTrpProAspHis 196
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                                                                                                                                                    280 AAGATTCAGACTATATCAATGCAAATTTTATAAAGGGGGTCTATGGGCCA 329
                                                                                                                                                                                                                                                                                                     LysAlaTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAspPh 113
                                                                                                                             eLeuProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAspG 80
                                                                                                                                                                                                                80 luAspSerSerTyrIleAsnAlaAsnPheIleLysGlyValTyrGlyPro 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gCysTyrGlnGluAspAspSerValProIleCysIleHisCysSerAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      877 AIGAACTIGITCAIAGAGCIATIGCCCAACIGITIGAAAAACAGCIACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGl
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1055 351	1099	149	68 199 ·	84 249	87 299	402 1349	419 1387	426 1437	433	450 1537	462 1587	72 537	489 1675 ·	500 1725	516 1775	533 1801	550 1847	55
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linear ROD 18-SEP-1995
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Charest, A., Wagner, J., Shen, S.H. and Tremblay, M.L. Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyrosine phosphatase Biochem. J. 308 (Pt 2), 425-432 (1995)
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Submitted (01-MAY-1995) M.L. Tremblay, McGill University, Dept of
Biochemistry, 3655 Drummond, Montreal, Quebec H3G 1Y6, CANADA
Related sequences: X64440 and S36169.
Location/Qualifiers
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                                                                                                                                                                                             599 lnGluSerAlaValLeuAlaThrAlaProArg.....IleAsp
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Tremblay, M.L.
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|1453 CCGTTACCACTGTGTGGCAGGACAGTGACAGGTACCACCCAAAGCCAGTG 1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1177 ATGAACTTGTTCATAGGGCTATTGCTCAACTGTTTGAAAAACAGCTACAA 1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 rGluSerGlnAlaLysHisCysIleProGluLysAsnHisThrLeuGlnA 322
                                                                                                                                                                                                                                                             AspValProSerSerIleAspProIleLeuGluLeuIleTrpAspValAr 213
780 GGAGAAGATCCTATAACATTTGCACCATTTAAAATTTCTTGTGAAAATGA 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ...GluIleSerAlaLysGluGluLeuValLeuHisProAlaLysSerSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 GlyGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGl 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eTrpArgMetileTrpGluTyrSerValLeuIleIleValMetAlaCysM 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 ysLeuLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThr 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 sLysIleThr.....LysGluGluPheAlaAsnGluPheLeuL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eLeuProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAspG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 ThrValAlaGluAsnAlaLysAsnIleLysLysAsnArgTyrLysAspIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysAlaTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAspPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
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ORIGIN
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411

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6761		עכ
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2169		205
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588	3 4	7
2253		Ö
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, ,		'nι
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9		
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PAT 11-DEC-2001
                                                                                                                                     house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                    Individual Control of the School Juridical Person (JP)

School Juridical Person Nihon University (JP)

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 GlyGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaG1 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 GCCACTGGAGAAAAAGAAAATGTTAAAAAGAACAGATATAAAGACAT 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 ThrValAlaGluAsnAlaLySAsnIleLySLySAsnArgTyrLySASpIl 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 eLeuProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAspG 80
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        ACCESSION
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        KEYWORDS
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ORIGIN
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AUTHORS
TITLE
JOURNAL
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Den Hertog,J.
                                                                                                                                           Direct Submission
Submitted (03-DEC-1991) J. den Hertog, Hubrecht Laboratory,
Netherlands Institute for Developmental Biology, Uppsalalaan 8,
3584 Ct Uthrecht, THE NETHERLANDS
2 (bases 1 to 2981)
den Hertog, J., Pals, C.E., Jonk, L.J. and Kruijer, W.
Differential expression of a novel murine non-receptor protein
tyrosine phosphatase during differentiation of P19 embryonal
                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 184 (3), 1241-1249 (1992)
92272714
M.musculus mRNA for P19-protein tyrosine phosphatase.
X63440 S36169
X63440.1 GI:416181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 743
Gaps: 22
Percent Identity: 35.935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 t
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52. .2373
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                                                                                                                                                                                                                                                                 carcinoma cells
                                                                            Mus musculus
                                                                house mouse.
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        DEFINITION
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ORGANISM
                    ACCESSION
VERSION
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MEDLINE
FEATURES
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AUTHORS
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TITLE
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251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGl
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 1049 AAGCCGCCGCGGACTCGAAGTTGCCTTGTAGAAGGGGGATGCCAAGGAAGA	306 GluSerGlnalaLysHisCysIleProGluLysAsnHisThrLeuGlnal::::: ::: :::	322 aASpSerTyrSerProAsnLeuProLysSerThrThrLysAlaalaLysM	339 ethetAsn 	342 GlnGlnArgThrLysMetGluIleLysGluSerSerSerPheAspPheAr	358 gThrSerGluIleSerAlaLysGluGluLeuValLeuHisProAlaLysS 281 GACCAATGGGGCAAAAA	375 erSerThrSerPheAspPheLeuGluLeuAsnTyrSerPheAspLysAsn 	392 AlaaspThrThrMetLysTrpGlnThrLysAlaPheProIle	405	1380 GCCCAAAAGTTTTGATGGGAACACTCTTGAATAGGGGACATGCGATTA	406ValGlyGluProLeuGlnLysHisGln	415 SerLeuAspLeuGlySerLeuLeuPheGluGlyCysSerAsnSerLysPr::: :::	431 oValAsnAlaAlaGlyArgTyr	439PheAsnSerLysValProlleThrargThrLysSerThrPro	453 PheGluLeuIleGlnGlnArgGluThrLysGluValAspSerLysGluAs :::::	469 nPheSerTyrLeuGluSerGlnProHisAspSerCysPheValGluMetG	486 InalaGlnLysValMetHisValSerSeralaGluLeuAsnTyrSerLeu ::::: :::	503 ProTyrAspSerLysHisGInIleArgAsnAlaSerAsnValLysHisHi ::::::	519 sAspSerSerAlaLeuGlyValTyrSerTyrIleProLeuValGluAsnP	536 roTyrPheSerSerTrpProProSerGly

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YQTKEQYELVHRAIAQLEFPHPVPILITPSPPSAFPTLHCVARQ"
347 c 361 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATRKPTP 1608 bp mRNA linear ROD 08-FEB-1999
Rat mRNA for protein tyrosine phosphatase, complete cds.
D38072
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Direct Submission

Direct Submission

Submission

Submission

Submission

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Submission

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Submission

School, 1st Dept. of Medicine; 2-2 Yamadaoka, Suita, Osaka 565,

Japan (Tel:06-879-3632, Fax:06-879-3639)

Chases I to 1608)

Moriyama, T. Kawanishi, S. Inoue, T., Imai, E., Kaneko, T., Xia, C.,

Takenaka, M., Noguchi, T., Kamada, T. and Ueda, N.

CDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP)

From rat kidney

Fress Lett. 353 (3), 305-308 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein tyrosine phosphatase.
Rattus norvegicus (strain:Sprague-Dawley) kidney cDNA to mRNA,
clone:RKPTP.
                                                                                                                                                                                                                                                                                                1946 CCAGTAGTGCTGAGAGT ...GCTTGCCATAGGAGAGTATTGCCGATGTCC 1992
                                                                                                                                                                                                                                                                                                                                                                                                         1826 CCCTCAGCTTTACCAACCCTCTTCACTCGACGACTGGCACTCAGACGGA 1875
                                                                                                         1876 GGGAGCTCT.....GATGGTGCTGT 1895
                                                                                                                                                                                                               1896 GACCAGGAACAAAACTAGCATTTCAACAGCAAGTGCCACAGTGTCTCCTG 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2034 TGAGAAAGATGCTGATGTTAGTGAGGAGTCGCCTCCTCCTTTACCTGAAC 2083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 .....IleAspAspGluIleProProProLeuProValA 621
                                                    546 ThrSerSerLysMetSerLeuAspLeuProGluLysGlnAspGlyThrVa 562
                                                                                                                                                             562 lPheProSerSerLeuLeuProThrSerSerThrSerLeuPheSerTyrT 579
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/db_xref="G1:699627"
                                                                                                                                                                                                                                                                                                                                                                           596 LeuLeuAsnGlnGluSerAlaValLeuAlaThrAlaProArg......
                                                                                                                                                                                                                                                                       579 yrAsnSerHisSerSerLeuSerLeuAsnSerProThrAsnIleSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Sprague-Dawley"
/db.xref="taxon:10116"
/clone="RKPTP"
/tissue_type="kidney"
135. .1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2084 GAACTCCTGAGTCTTTTGTATTAGCAGAT 2112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 rgThrProGluSerPheIleValValGlu 630
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ORIGIN

us-09-600-358a-4.rge

uLysArgLysSerAspTyrIleIleArgThrLeuLysValLysPheAsnS 180 234 284 334 eTrpArgMetIleTrpGluTyrSerValLeuIleIleValMetAlaCysM 130 534 163 684 AspValProSerSerIleAspProIleLeuGluLeuIleTrpAspValAr 213 gCysTyrGlnGluAspAspSerValProIleCysIleHisCysSerAlaG 230 834 46 80 30 63 96 1 MetAspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17 185 GAAAAGTCCGGACCACAATGGGGAGGACAACTTCGCCCGGGACTTCATGC 17 sLysIleThr.....LysGluGluPheAlaAsnGluPheLeuL ysLeuLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThr 80 luAspSerSerTyrIleAsnAlaAsnPheIleLysGlyValTyrGlyPro eLeuProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAspG 635 ACAAGCAAGAACAGACTACTTCATTCGAACACTTTTACTTGAATTTCAAA GlyGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGl Length: 465 Gaps: 12 Percent Identity: 47.742 to: 1608 from: 1 Align seg 1/1 to: RATRKPTP Ratio: 3.112 Percent Similarity: 73.118 US-09-600-358A-4 x RATRKPTP Quality: 1058.00 alignment_scores alignment_block 163 30 63 97 435 113 213 197 147

|| ||| ||| :::||| |||| |||::::: 1132 CTCCAAAGCCACCACGACTCGAAGTT...GTCTTGTAGAGGGGGTGCC 1178 : :::::|||||||: 1329 GCCCCCAACG........GACCTCAACAGAAACTAIGAFAAGT 1363 1414 AAGTTAGAACAAAATTTAAGTTTTGAGATTAAGAAAGTCCCTCTCCAAGA 1463 1229 GACACCGTCGCTCCTTCAGCATTCCCAACGTTACACTGTGTGGCCAAGAC 1278 1279 AGTGACAGGTACCACCCAAAGCCAGTGCTGCACATGGCTTCCCCAGAGCA 1328 1364 CAGCGGACCTAATGGGGAGAAGCGAATCTGCTGTTGAGCACACAGATAAA 1413 1032 CTGTATGAAATCCACGGAGCCCAGAAAATCACTGATGGTAATGAAATTAG 1081 345 360 396 280 296 314 374 391 397 LysTrp...GlnThrLysAlaPheProlleValGlyGluProLeuGlnLy 412 931 981 346LysMetGluIleLysGluSerSerSerPheAspPheArgThrSer 374 sSerSerThrSerPheAspPheLeuGluLeuAsnTyrSerPheAspLysA 280 yrGluLeuValTyrAsnAlaValLeuGluLeuPheLysArgGlnMetAsp 303SerGlyThrGluSerGlnAlaLysHisCysIleP 330 oLysSerThrThrLysAlaAlaLysMetMetAsnGlnGlnArgThr.... 1082 CACTGGAAACATGGTCAGTTCCATTGATAGTGAAAAACAAGATTCTCCTC 314 roGluLys. AsnHisThrLeuGlnAlaAspSerTyrSerProAsnLeuPr 1179 AAGGAAGAAATCCTCCAGCCACCAGCCTCACCCGGTGCCGCCCATCCT 361 GluIleSerAlaLysGluGluLeuValLeuHis.....ProAlaLy snAlaAsp....ThrThrMet LeuLeuLysAspGlyIleIleProGluAsnPheSerValPheSerLeuIl 932 ACAAGAAATGAGAACACAAAGGCACTCTGCAGTACAAACGAAGGAGCAGTIleArgAspLysHis..... s...HisGlnSerLeuAspLeuGlySerLeuLeuPheGluGly 425 297 Val..... 247 263 391 412

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TYPE: nucleic acid
STRANDEDNESS: single
   Query Match
Best Local Similarity
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US-09-081-345-1
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US-09-081-345-1
(without alignments)
6071.260 Million cell updates/sec
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1 tcctcaacctacttataga......cctagtcggagcacatccgg 2356
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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                                                                     Compugen Ltd
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                                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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CLASSIFICATION ON:

PRIOR APPLICATION NUMBER: 60/047,222

RELING DATE: May 20, 1997

FILING DATE: May 20, 1997

FILING DATE: May 20, 1997

ATTORNEY-AGENT INFORMATION:
NAME: WATDURY, RICHARD J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 334/253

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TELEPHONE: (213) 489-1600

TELEPHONE: (213) 955-0440

TELEPHONE: (213) 955-0440

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US-08-548-164-2
US-08-015-973-2
US-08-015-973-2
US-08-94-308-1
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Pred. No. 0;
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTE READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRASISED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,345
FILING DATE: Herewith
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0; Conservative 0; Mismatches 4; Indels 3; Gaps ctoaacctacttatagactattttcttgctctgcagcatggaccaaagagaaattc 60	gaagttootggatgaggoocaaagoaagaaattaotaaagaggagttgooaatg 1	.ttctgaagctgaaaaggcaatctaccaagtacaaggcagacaaaacctatcctacaa 180	ggctgagaatgccaagaatatcaagaaaacagatataaaggatattttgccctatg 240	tagccgggtagaactatccctgataacctctgatgaggattccagctacatcaatg 300	ccacttcattaagggagtttatggacccaaggcttatattgccacccaggtcctttat 360	ttacaaccctcctggacttctggagatgatttgggaatatagtgtccttatcattgtta 420	catgcatggagtatgaaatgggaaagaaaagtgtgagcgctactgggctgagccag 480	agatgcagctggaatttggccctttctctgtatcctgtgaagctgaaaaaggaaat 540	attatataatcaggactctaaaagttaagttcaatagtgaaactcgaactatctacc 600	toattacaagaattggccagaccatgatgtaccttcatctatagaccctattcttg 660	tcatctgggatgtacgttgttaccaagaggatgacagtgttcccatatgcattcact 720	tgetggetgtggaaggaetggtgttatttgtgetattgttgattatacatggatgt 780	otaaaagatgggataattcctgagaacttcagtgttttcagtttgatccgggaaatgc 840	icacagaggccttcattagttcaaacgcaggaacaatatgaactggtctacaatgctg 900	tagaactatttaagagacagatggatgttatcagagataaacattctggaacagaga 960	agcaaagcattgtattcctgagaaaatcacactctccaagcagactcttattctc 1020	tttaccaaaagtaccacaaaagcagcaaaatgatgaaccaacaaaggacaaaa 1080
ches 2090	61 tgcaq	121 aatt	181 ctgtg	241 attat	301 cca	361 cta	421 tggc	481 gaga	541 ctg	601 agtti	661 agc	721 gcag	781 tgc	841 gga	901 tat	961 gtcaagc	1021 ctaatt
1 tccc											111						
12 TCC	72 TGCAC	132 AATT	192 CTGTG	252 ATTA1	312 CCA	372 CTA	432 TGGC	492 GAG		612 AGTT	672 AGC	732 GCAG	789 TGC	849 GGA	909 TAT	969 GTCAAGC	1029 CTAAT
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RESULT 2 US-08-821-278A-1 ; Sequence 1, Application US/08821278A

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                                                                                                                                                                                                                                                                             243 ttccctgctccaagaggaggacatggaaattacatcaatgccaacttcatccggggcat 302
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         GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: Protein Tyrosine Phosphatases
FILE REFERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 23
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                                                                                                                                           ; TYPE: DNA
; ORGANISM: Mus musculus
US-08-821-278A-1
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Matches 410; Conserv
6238902
                                                                                                                 SEQ ID NO 1
LENGTH: 1529
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US-08-951-260A-1
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267 ataaccictgatgaggattccagctacatcaatgccaacttcattaagggagtttatgga 326
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APPLICANT: AOKI, NAONITO
APPLICANT: Ullitch, AAC.
TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 214.2; DB 3;
Pred. No. 9.3e-50;
0; Mismatches 298;
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,260A
FILING DATE: October 16, 1997
CLASSIFICATION 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,860
FILING DATE: NO. 6004791ember 13, 1996
APPLICATION NUMBER: PCT/1897/00946
                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: June 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: WATHING
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                           ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 57.4%;
Matches 406; Conservative (
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 2226 base pairs
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STRANDEDNESS: single
                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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US-08-036-210-10
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                          TGCATCACCCTGACAAAGGAGACAGCACTGACTTCGGACATCACTCTCAGGACCCTCCAG
                                                                                 catgatgtaccttcatctatagaccctattcttgagctcatctgggatgtacgttgttac
                                                                                                                                                                                                                            739 GTCTTGTGTGC---TGTTGATTACGTGAGGCAGTTGCTTCTGACTCAGACAATCCCACCC
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OTHER INFORMATION: /note= "N=x=unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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1155 Avenue of the Americas
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FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MOller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ulrich, Axel
TITLE OF INVENTION: PTP-S31: A NOY
TITLE OF ENVENTION: PTSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08036210 Patent No. 5585233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,812
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-z/11
COMPUTER READABLE FORM:
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ZIP: 10036-2711
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STREET: 11
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US-08-036-210-10
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                                                                                             tcctacaactgtggctgagaatgccaagaatatcaagaaaaaagatataaggatattt 232
                                                                                                                          teetttatetacaaceeteetggaettetggaggatgatttgggaatatagtgteettat 412
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    Length
                                                Indels
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Score 130.6; DB 1;
Pred. No. 1.5e-26;
0; Mismatches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08449609
Patent No. 5952212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTP-S31: A PHOSPHATASE
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21P: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-531:
TITLE OF INVENTION: PHOSPHATA
  Query Match 5.5%;
Best Local Similarity 51.1%;
Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-449-609-10
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724 TGTTCACTGCAGTGCTGGAGTTGGAACACTGGAGTTTTTATTGCTCTGGACCATTTAAC 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               687 TATTAATGCCAGCTATATTCTGGTTATTTATGTCCAAATGAATTATTGCTACTCAAGG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 teetttatetacaaeceteetggaettetggaggatgatttgggaatatagtgteettat 412
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                                                                                                                                                                                                                                                                                                                             PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2149
OTHER INFORMATION: /note= "N=x=unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 130.6; DB 1;
31.1%; Pred. No. 1.6e-26;
1ve 0; Mismatches 294;
                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 Sequence 14, Application US/08036210 Patent No. 5585233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 51.1%;
Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                          US-08-036-210-14
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                                              773 a 773
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Pred. No. 1.5e-26;
0; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 1766
; OTHER INFORMATION: /note= "N-x-unknown nucleotide"
US-08-449-609-10
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
ELLING DATE: 23-WAR-1993
ATTORNEY/AGENT INFORMATION:
                                                              APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                     ALTURAL TOWN.

NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2309 base pairs
TYRE: nucleic acid
STRANDENNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                    FILING DATE: 2, CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: un
MOLECULE TYPE:
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                                                              tgagccaggagagatgcagctggaatttggccctttctctgtatcctgtgaagctgaaaa 532
                                                                                                                                         867 AGAGGACAACAAGCCAGTTACTGTCTTTGGAGATATAGTGATTACAAAGCTAATGGAGGA 926
                                                                                                                                                                                       tatctaccagtttcattacaagaattggccagaccatgatgtaccttcatctatagaccc 652
                                                                                                                                                                       533 aaggaaatctgattatataaatcaggactctaaaagttaagttcaatagtgaaactcgaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7683-025
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Patent No. 5952212
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullitch, Axel
TITLE OF INVENTION: PTP-S31: A
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18,872
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TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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1047 TCTAATTCACTTGTGAAGTTGGTTCGAGCAAGCAGGGCACATGACCACCACCTATGAT 1106
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                                                                                                                                                                                                                                                                                                                                                                              catcaatgccaacttcattaagggagtttatggacccaaggcttatattgccacccaggg
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                                                                                                                                                                                                      Length 2692;
                                                                                                                                                                                                      Score 130.6; DB 2; Length
Pred. No. 1.6e-26;
0; Mismatches 294; Indels
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                                                                                 Sequence 21, Application US/08036210 Patent No. 5585233 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MOIler, Niels P.H. APPLICANT: MOIler, Karin B. APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENNIE & EDMONDS
                                                                                                                                                                                                        Similarity 51.1%;
                                                                                                                                                                                                                                             Matches 307; Conservative
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TITLE OF INVENTION: PHOS
NUMBER OF EXCUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE 6 EI
nucleic acid
                                      TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
                     STRANDEDNESS:
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2328 TCTAATTCACTTTGTGAAGTTGGTTCGAGCAAGCAGGCACATGACACCACACCACACATGAT 2387
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OTHER INFORMATION: /note= "N=x=unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
RICHARD APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.5%; Score 130.6; DB 2;
31.1%; Pred. No. 2e-26;
ve 0; Mismatches 294;
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1155 Avenue of the Americas
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      US-08-449-609-21
Sequence 21, Application US/08449609
Petent No. 5952212
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                             PTP-S31: A PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/OOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18,872
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REGISTRATION NUMBER: 18,8
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LOCATION: 3430
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Best Local Similarity 51.1%
Matches 307; Conservative
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ADDRESSEE: PENNIE &
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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Pred. No. 2e-26;
0; Mismatches 294; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "N=x=unknown nucleotide"
                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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1155 Avenue of the Americas
                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                    COMPUTER REDABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 3973 base pairs
                                                                                                                                                                                                                                                                                                                                                                                         212-869-8864/9741
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                                                                                                                                                                                          CURRENT APPLICATION DATA:
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LOCATION: 3430
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Best Local Similarity 51.1
Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                       XY: U.S.A.
10036-2711
                                       New York
                      New York
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                                                       COUNTRY:
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FILING DATE:
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LOCATION:
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                                                                     1968 TATTAATGCCAGCTATATTTCTGGTTATTTATGTCCAAATGAATTTATTGCTACTCAAGG 2027
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                                                                                                  353 tcctttatctacaaccctcctggacttctggaggatgatttgggaatatagtgtccttat 412
                                                                                                                                                                                                                                                                             533 aaggaaatctgattatataatcaggactctaaaagttaagttcaatagtgaaactcgaac 592
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                                                                                                                                                             593 tatctaccagtttcattacaagaattggccagaccatgatgtaccttcatctatagaccc
                                          catcaatgecaacttcattaagggagtttatggacccaaggcttatattgccacccaggg
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Best Local Similarity 62.8%; Pred. No. 5.9e-24;
Matches 186; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORDATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: Protein Tyrosine Phosphatases; FILE REPERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 16
LENGTH: 466
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Best Local Similarity
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US-08-821-278A-16
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236 tggatggaagcctggcctacattgccacgcaaggacccttgcctcacaccctgctagact 295
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
                                           tctggagactggtctgggagtttggggtcaaggtgatcctgatggcctgtcgagagatag
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                                                                                                                            Length 5117;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray 6 STREET: 233 South Wacker Drive, Suite 6300 CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
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0; Mismatches 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicayo
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
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APPLICATION NUMBER: US/08/237,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-6448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5117 base pairs
                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08854585
Patent No. 6114140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: BOTUN MICHAEL F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 388; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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350..4364
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                            3690 GACCTTTACCGAACACTTTGAAAGATTTTTGGCGTATGGTTTGGGAGAAAATGTATATG 3749
                                                                                 3810 CCTCCAAGCAGGCTCAGGACTATGGAGACATAACTGTGGCAATGACATCAGAAATTGTTC 3869
                                                                                                                                                                                                                     3870 TTCCGGAATGGACCATCAGAGATTTCACAGTGAAAAATATCCAGACAAGTGAGAGTCACC 3929
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                                                                                                                                                                                                                                                                                                                                                                                                                                              766 attatacatggatgttgctaaaagatgggataattcctgagaacttcagtgttttcagtt 825
                                                                                                                          ctgagccaggagagatgcagctggaatttggccctttctctgtatcctgtgaagctgaaa 531
                                                                                                                                                                                       532 aaaggaaatctgattatataatcaggactctaaaagttaagttcaatagtgaaactcgaa 591
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352 gtcctttatctacaaccctcctggacttctggaggatgatttgggaatatagtgtcctta 411
                                                             4218 TCCTCAATCAGTGTGTTTTGGATATTGTCAGATCCCAGAAAGACTCAAAAGTAGAT 4273
                                                                                                                                                                                                                                                                                                                652 ctattcttgagctcatctgggatgtacgttgttaccaagagga-----tgacagtgttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tooks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
UNDBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
ADDRESSEE: Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: PCT/US95/05512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application PC/TUS9505512 GENERAL INFORMATION:
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REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
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3513 AACCTAAATATGCAGCAGAACTGGCTGAGAATAGAGGAAAGAATCGCTATAATAATGTTC 3572
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                                                                                                                                                                                                                                             Length 5117;
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                                                                                                                                                                                                                                         Score 116.8; DB 5;
Pred. No. 1.5e-22;
0; Mismatches 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08241853
Patent No. 5693488
                                                                                                                                                                                                                                         Query Match 5.0%;
Best Local Similarity 50.0%;
Matches 388; Conservative
                   5117 base pairs
SEQUENCE CHARACTERISTICS:
                               nucleic acid
                                                                                                                                       CDS
350..4364
                                                                                                 MOLECULE TYPE: CDNA
                                                                              linear
                                    TYPE: nucleic
STRANDEDNESS:
                                                                            TOPOLOGY:
                                                                                                                                         NAME/KEY:
                                                                                                                                                        ; LOCATION:
PCT-US95-05512-1
                   LENGIH:
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2181 GTACGGGCCATCAATGGAGAATGGCTCTGCAACATATGGGGACATAACTGTGAAGATCAA 2240
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Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,917
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/241,853
FILING DATE: 12-MAY-1994
ATTORREY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Klauber & Jackson
411 Hackensack Avenue
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New Jersey
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STREET: 41
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                        APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER VIOLATION OF A STATE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE: ORGANISM: Gallus domesticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5801
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3969 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                   E: Klauber & Jackson
411 Hackensack Avenue
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Best Local Similarity 49.3°
Matches 336; Conservative
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CITY: Hackensack
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GENERAL INFORMATION:
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US-08-241-853-1
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Pennsylvania Avenue, N.W.

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ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2241 CGAAAGTAAAATATGTCCAGACTATATAATTCAGAAACTGCACATCACAAATGGAAGGA 2300
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                                                                                                                                                                                                                                                                                                                                                                                                                  cacccagggtcctttatctacaaccctcctggacttctggaggatgatttgggaatatag 403
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                                                                                                                                                                                                                      164 caaaacctatcctacaactgtggctgagaatgccaagaatatcaagaaaaacagatataa 223
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Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
                                                                                                                                                                                        6
                                                                                                                                                       Length 3969;
                                                                                                                                                                                          Indels
                                                                                                                                                       Score 115.4; DB 2;
Pred. No. 3.2e-22;
0; Mismatches 336;
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                            ORGANISM: Gallus domesticus
STRAIN: DT40
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Best Local Similarity 49.3%;
Matches 336; Conservative
                                                                         CDS
91..3802
             ORIGINAL SOURCE
                                                                       ; NAME/KEY:
; LOCATION:
US-08-850-917-1
ANTI-SENSE:
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Pred. No. 2.9e-20;
0; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                0A146-0110
                                                                                                               SOFTWARE: FRATESE DOS
SOFTWARE: FRATESE VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION .
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTONNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May 26, 2002, 10:33:59 Job time: 12816 sec
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                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 0P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 64.4%;
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 247 base pairs
TYPE: nucleic acid
                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-639-7890
             STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
Washington
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MOLECULE TYPE: CD
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ORIGINAL SOURCE:
US-08-594-031-74
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V86781 W.musculus D38072 Rat mRNA fo AX306312 Sequence X63440 W.musculus U69700 Human prote U49853 Mus musculu U35124 Mus musculu U5253 Mus musculu

Scoring table:

Searched:

Minimum Maximum

OM nucleic

Run on:

AR154418 Sequence BC008512 Mus muscu U69673 Rattus norv

AR095603 Sequence X79568 H. saptens B Y00062 Human mRNA M14342 Mouse 200 k M14343 Mouse Ly-5 M92933 Mouse Ly-5 M0072 Rat leukocy Y00055 Rat mRNA fo AR073853 Sequence

132037 Sequence 10 AR073854 Sequence 132038 Sequence 14 AR073855 Sequence

132039 Sequence 21 AF173857 Xenopus 1 AR154432 Sequence D37781 Human mRNA AR109903 Sequence U10886 Human densi

X58287 Murine mR-P U40790 Rattus norv

07-SEP-2000

PAT

linear

/note="unnamed protein product"
/codon_start=1

CDS

Description

Query Match Length DB

Score

Result

ART01846 Homo sapi ART49916 Sequence ART50732 Homo sapi M90388 Mouse prote AL137856 Human DNA BC017785 Homo sapi M93425 Human prote D13380 Human mRNA G18337 SWSS1985 Er

Sequence Homo sapi Sequence Homo sapi

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Eukaryoptusis Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 2356)
Roifman,C.M. Human lymphoid protein tyrosine phosphatases Patent: WO 9936548-A 3 22-JUL-1999; HSC RES DEV LP (CA); ROIFMAN CHAIM M (CA)
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                                                        6 AX020261
9 AF001846
6 AR149916
9 AF150732
10 MUSPROTYPH
9 AL137856
9 BC017785
9 HUMPTPPEST
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Sequence 3 from Patent WO9936548.
AX020263
AX020263.1 GI:10044044

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    /organism="Homo sapiens"
/db_xref="taxon:9606"
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MAMPTPPES

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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                (without alignments)
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1 teceteaacetaettataga......cetagteggageacateegg 2356
                                                                                                                                                                                               May 26, 2002, 06:59:45; Search time 5560.98 Seconds
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                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
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                                                                                                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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DB seq length: 2000000000
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 2556)

Cohen,S., Dadi,H., Shaoul,E., Sharfe,N. and Roifman,C.M.

Cloning and characterization of a lymphoid-specific, inducible human protein tyrosine phosphatase, Lyp

Blood 93 (6), 2013-2024 (1999)
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Sick Children, 555 University Avenue, Toronto, Ontario M5G 1X8,
                                                  ctccaaggatagatgatgaaatccccctccacttcctgtacggacacctgaatcattta
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Roifman, C.M.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 3058)
Roifman, C.M.
Human I ymphoid protein tyrosine phosphatases
Patent: WO 9936548-A I 22-JUL-1999;
HSC RES DEV LP (CA); ROIFWAN CHAIM M (CA)
Location/Qualifiers
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1200 1500 1740 1980 2040 gtcaagcaaagcattgtattcctgagaaaaatcacactctccaagcagactcttattctc attettacatacettagtggaaaateettatttteateatggeeteeaatggtacea ATTCTTACATACCTTTAGTGGAAAATCCTTATTTTTCATCATGGCCTCCAAGTGGTACCA ggaccaaatcaactccttttgaattgatacagcagagaaaccaaggaggtggacagca aggaaaacttttcttatttggaatctcaaccacatgattcttgttttgtagagatgcagg CTCCAAGGATAGATGATGAAATCCCCCTCCACTTCCTGTACGGACACATGATTA ctccaaggatagatgatgaaatccccctccacttcctgtacggacacctgaatcattta ttgtggttgaggaagctggagaattctcaccaaatgttcccaaatccttatcctcagctg tgaaggtaaaaaattggaacatcactggaatggggtggaacatctgaaccaaagaaatttg 1081 1081 1141 1201 1261 1381 1381 1441 1501 1561 1621 1681 1021 1141 1321 1321 1441 1501 1561 1741 1741 961 1021 1201 1261 1621 1681 1801 1801 1861 1861 1921 1921 1981 1981 961 g δ d οy g οy qq δ g Q QQ οy g οχ g òγ g δ g δ g Q g Ω a ò g δý qq οy g δ g g à

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3058)
Cohen,S., Dadi,H., Shaoul,E., Sharfe,N. and Roifman,C.M.
Cloning and characterization of a lymphoid-specific, inducible human protein tyrosine phosphatase, Lyp
Blood 93 (6), 2013-2024 (1999)
                                                                                                                                                                                    Submitted (30-APR-1997) Immunology and Allergy, The Hospital For Sick Children, 555 University Avenue, Toronto, Ontario MSG 1X8, Canada
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Roifman, C.M.
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Jallal, B. and Plowman, G.D.
Diagnosis and treatment of PTP04 related
Patent: US 6228641-A 1 08-MAY-2001;
Location/Qualifiers
1. 3580
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6228641.
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AR149916
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HEWPARAFOIVGSSEASKLWASLCLGASNSNINCSCRIPRPFCOYPDOINSFELIQ
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SKSLKILRNMKKSICNSCPPNKPAESVQSNNSSSFLNFGFANRFSKFRGPRPPTWN
                                                                                                                                         AFISO732 2877 bp mRNA linear PRI 04-MAY-2000
Homo sapiens protein tyrosine phosphatase (PTP) mRNA, complete cds.
AFISO732
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Zhangjiang Hi-Tech Park, Pudong,
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostor
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2877)
Huang,C., Zhang,C., Wu,T., Peng,Y., Gu,Y., Zhang,L., Jiang,C.,
Li,Y., Han,Z., Wang,Y., Chen,Z. and Fu,G.
A novel gene expressed in human adrenal gland
Unpublished
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Huang,C., Zhang,C., Wu,T., Peng,Y., Gu,Y., Zhang,L., Jiang,C., Li,Y., Han,Z., Wang,Y., Chen,Z. and Fu,G.

Direct Submission
Submitted (12-MAY-1999) Chinese National Human Genome Center a Shanghal, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudo Shanghal, 201203, P. R. China

Location/Qualiflers

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RESULT 7 MUSPROTYPH LOCUS

2/34 pp mRNA linear ROD 27-APR-1993 phosphatase (702pep) mRNA, complete cds. Mouse protein tyrosine pi M90388 M90388.1 GI:200522 protein-tyrosine phosphat Mus musculus CDNA to mRNI Mus musculus Eukaryota; Metazoa; Chorr Mammalia; Eutheria; Roder MUSPROTYPH

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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus Chordata; Rodentia;

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              Matthews, R.J., Bowne, D.B., Flores, E. and Thomas, M.L. characerization of hematopoietic intracellular protein tyrosine phosphatases: Description of a phosphatase containing an SH2 domand another eriched in proline-, glutamic acid-, serine-, and
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                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                           113. .2521
/gene="70zpep"
/EC_number="2.7.1.112"
/codon_start=1
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/organism="Mus
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113. .2521
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Best Local Similarity 77.3%;
Matches 1637; Conservative
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gcagtgctggctgtggaaggactggtgttatttgtgctattgttgattatacatggatgt
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On Jul 19, 2001 this sequence version replaced gi:14586004.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
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P RP5-107303 on chromosome lp13.1-13.3,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143618)
                                                                                                                                                     1794 CCCCTGGCGCTCTATTGCCAGCCTCTTTACAACCTCCTTCTTTATAGCAACCCAGAGG 1853
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                                                   catatgactctaaacaccaaatacgtaatgcctctaatgtaaagcaccatgactctagtg
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                                                                                                      CTGGTGCCT------GTGATGCGTCGTGTGCCCCGGCACAGCCCCGGCG
                                                                                                                                                                                                                                                              caagtggtaccagttctaagatgtctcttgatttacctgagaagcaagatggaactgttt
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AL137856.24 GI:14970654
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assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL: Sw., SWISSEROT: Tr., TREMBL: WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 139. 237 of consensus"
12210. .12464
/note="Malusg repeat: matches 1. .291 of consensus"
12916. .13149
/note="MERS8B repeat: matches 70. .341 of consensus"
13150. .13435
/note="Aluss repeat: matches 1. .298 of consensus"
13458. .13805
/note="LIMD2 repeat: matches 4851. .5213 of consensus"
13458. .13806
/note="LIM15
/note="Aluss repeat: matches 1. .299 of consensus"
14118 .14130
                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                    This sequence is the entire insert of clone RP5-107303 The true right end of clone RP1-215C20 is at 30467 in this sequence. The true right end of clone RP11-324J2 is at 119169 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1. .298 of consensus" 9793. .10559
/note="L1MC1 repeat: matches 5526. .6320 of consensus" 10574. .10730
                                                                                                                                                                                                                                            http://www.sanger.ac.uk/HGB/Chr1
RP5-107303 is from the library RPCI-5 constructed by the group
Pieter de Jong. For further details see
http://www.chri.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6522. .5927 **
Anote="LIME repeat: matches 5524. .5813 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches 2655. .2705 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER5A repeat: matches 41. .109 of consensus"
and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluSx repeat: matches 1. .312 of consensus"
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11220. .11315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2655. .2705 of consensus 2305. .246
/note="MIR repeat: matches 40. .176 of consensus" 5652. .5927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .139 of consensus"
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/note="BC200 repeat: matches 2, .147 of cons 6553, .6700
7005="8 Copies 6 mer acacac 97% conserved" 7925, .7980
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/note="AluSx repeat: matches 1. .296 of 9048. .9342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2417
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1919. .1969
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10759. .10907
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10908. .11219
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14910 .15215 /note="LiMD2 repeat: matches 53025609 of consensus"	/note=") 16270.	/note="MIR repeat: matches 4 1684017032		_			/note="AluSx repeat: matches 1306 of consensus 2327523506	/note="AluJb repeat: matches 1225 of consensus 2354023584	/note="L2 repeat: matches 26472694 of consensus" 2359023671	/note="AluJ/FLAM repeat: matches 1 2371424013	/note="	/note="	/note="		2812328115 /note="LZ repeat: matches 26782733 of consensus"		-	29767. /note="	3005330345 /note="L2 repeat: matches 24482750 of consensus"	31191 /note="A	3205 /not	32503. /note="?		32817 /note="A	3315633450 /note="AluJb	3374734055 / note="Aluxa5 repeat: matches 1309 of	3458434775 /note="LIME repeat: matches 56445823 o	3478634930
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/note="LiMH5 repeat: matches 5921. .6142 of consensus" 39036. .39268
/note="MIR repeat: matches 20. .262 of consensus" 39278. .39564
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/note="1.1NE repeat: matches 5265. .5563 of consensus" 35577. .35727
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 36 Row: j Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15619016. Location/Qualifiers
1. .1817
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PTTVAEKPKNIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIAT
OGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKEAEKRKSDYIIRTLKVKFNSVSVI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                              44896 TTAGTGGAAAATCCTTATTTTCATCATGGCCTCCAAGTGGTACCAGTTCTAAGATGTCT 44837
                                                                                                                                                                                                                                                                   1817 bp mRNA linear Homo sapiens, clone MGC:22283 IMAGE:4666653, mRNA, BC017785 GI:17389491 MGC.
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                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
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RYYPTQGELANTVIDFRWANTWILDFPHSRVKLTLKTPSQDSDYINANFIKGYGFRA
YVATQGELANTVIDFRWANTWENVVIIVWACREFEMORKKCERYWPLYGEDFITFAPF
KISCEDEQARTDYFIRTLLLEFQNESRRLYOFHYVNWPDHDVPSSFPSILDMISLMRR
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YQTKEQYELVHRAIAQLFEKQLQIVEIHGAQKIADGVNEINTENMISSIEPEKQDSPP
PKRPRTRSCLVEGDAKEEILQPPEPHPVPPILIPSPPSAFPTVTVWQDNDRYHPKPV
LHWYSSEQHSADLMNYSKGTELPGKNESTIEOIDKKLERNISFEIKKVPLQECPKSP
DGNTILNRGHAIKIKSASPCIADKISKPQELSSDLNVGDTSQNSCVDCSVTGSPKVSV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human protein tyrosine phosphatase (PTP-PEST) mRNA, complete cds.
M93425
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Yang, O.C., Tonks,N.K. and Sommercorn, J.
Cloning expression of PTP-PEST: a novel, nontransmembrane
protein tyrosine phosphatase
                                                                                               1 teceteaacetacttatagaetatttttettgetetgeageatggaecaaagagaaatte
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Length 1817;
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Score 447.2; DB 9;
Pred. No. 1.6e-92;
0; Mismatches 3;
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30. .2372
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Homo sapiens
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99.3%;
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YOARGEPLANTVIDEWRAWENVVIVANDEREENGRKCERYWPLYGEDPITFAPF
KISCEDEGARTDYFIRTLLEFONESRLYOFHYWWPDHDVPSSFDSILDMISLMRK
YOEHEDVPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEERWYFNIJOEMRTORHSA
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PREPRIATAQLEEROLADHYPPILLPPSPSPSAPPTYTWWODNDRYHPRPV
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TPPEESQNSDTPPRPDLYDLHDHWSPLRPTSCHVPLHSDSDSDSRNSDGAYTQNKTNI
STRSATVSAATSTESISTRKVLPMSIARHIAGTHRSGARKDVDVSEDSPPLFERTP
ESSFVLASSHWYPWSEWSELOSGRESGKRSGLITSENEKCDHPAGGIHYEMCIECP
PPTSSDKREDISENTTEATDIGFGNRCGKPKGPRDPPSEWT"
r PRI 23-JUN-1999 complete cds.
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                                                                                                                        PEST-domain phosphatase; leukocyte common antigen related molecule; protein tyrosine phosphatase G1. Homo sapiens adult colon cDNA to mRNA, clone_lib:Clontech. Homo sapiens
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1 (bases 1 to 2938)

Takekawa,M., Itoh,F., Hinoda,Y., Arimura,Y., Toyota,M., Sekiya,M., Adachi,M., Imai,K. and Yachih,A.

Cloning and characterization of a human cDNA encoding a novel putative cytoplasmic protein-tyrosine-phosphatase

Biochem. Blophys. Res. Commun. 189 (2), 1223-1230 (1992)
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Submitted (09-OCT-1992) to DDBJ by:
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/product="protein tyrosine phosphatase/protein.id="BAAQ0568.1"
/db_xref="G1:220034"
      HUMPTPG1 2938 bp mRNA linea
Human mRNA for protein-tyrosine-phosphatase Gl,
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Pred. No. 2.8e-76;
0; Mismatches 304;
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/clone_lib="Clontech"
/dev_stage="adult"
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Sapporo Medical College
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ilarity 65.1%;
Conservative
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Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 301402201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mapping project, see
Also see Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This STS was developed from sequence determined by anot investigator. See GenBank record: D13380 For additional information about the NHGRI chromosome 7 mapping project, http://www.nhgri.nih.gov/DIR/GTB/CHR7. Also see Genomics 11:548-64 (1991) [MUID=92128937].
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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100 mM
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Primer A: GTAAGAAATTCTGCATGG
Primer B: TTTTCTAAAACTCCAGGG
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2760. .2832
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/gene="PTPN12"
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PCR Cycles:
Thermal Cycler:
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Taq Polymerase:
Total Vol:
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Contact: Eric D. Green
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Annealing:
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                                                                                            Green, E.D.
Human chromosome 7
Unpublished
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Tris-HCl:
NH4Cl:
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GDB: GDB:3754375
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Homo sapiens STS genomic, sequence tagged
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2938)
Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F.,
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                                                                                             tattitgccctatgattatagccgggtagaactatccctgataacctctgatgaggattc
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                                                                                                                                                          217 CATACTGCCATTTGATCACAGCCGAGTTAAATTGACATTAAAGACTCCTTCACAAGATTC
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                                          aacctatcctacaactgtggctgagaatgccaagaatatcaagaaaaaagatataagga
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ESFVLADMPVNRFEWHELPNOEMSCORESEGLITGSGNEKHDAGGIHTEASADSPPAFSD
KRDQTTKSRAEVTDTGFGRRKGKPKGPREPPSEWT"

A 632 c 682 g 588 t
                                                                                        McGill University, Dept
Quebec H3G 1Y6, CANADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="protein-tyrosine-phosphatase"
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/db_xref="G1:804998"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.7%; Score 370.2; DB 10; Best Local Similarity 64.9%; Pred. No. 8.3e-75; Matches 587; Conservative 0; Mismatches 303;
                                                                     Direct Submission
Submitted (01-MAX-1995) M.L. Tremblay, 18 Submitted (01-MAX-1995) M.L. Tremblay, 18 Schemistry, 3655 Drummond, Montreal, 18 Sequences: X63440 and S36169.
Location/Qualiflers
1. 2676
/organism="Mus musculus"
Biochem. J. 308 (Pt 2), 425-432 (1995)
                                                                                                                                                                                                                                                         /mape"region A3-B"
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1. .14
                                                                                                                                                                                                                                                                                                                                  /note="synthetic linker"
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                                                                                                                                                                                                                                                                                                                                                                                                            /gene="mptp-pest"
/EC_number="3.1.3.48"
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/gene="mptp-pest"
330. .2657
                                                                                                                                                                                                         /strain="BALB/c"
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                                2 (bases 1 to 2676)
Tremblay, M.L.
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Charest, A., Wagner, J., Shen, S.H. and Tremblay, M.L.
Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyrosine phosphatase
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Submitted (26-AUG-1994) Toshiki Moriyama, Osaka University Medical Schmitted (26-AUG-1994) Toshiki Moriyama, Osaka University Medical School, 1st Dept. of Medicine; 2-2 Yamadaoka, Suita, Osaka 565, Japan (Tel:06-879-3632, Fax:06-879-3639)
Worlyama, T., Kawanishi,S., Inoue,T., Imai,E., Kaneko,T., Xia,C., Takenaka,M., Noguchi,T., Kamada,T. and Ueda,N.
CDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kidney
FEBS Lett. 353 (3), 305-308 (1994)
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Rattus norvegicus (strain:Sprague-Dawley) kidney cDNA to mRNA, clone:RRPPI and reserve strain:Sprague-Dawley) kidney cDNA to mRNA, sattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                   441 atgggaaagaaaaagtgtgagcgctactgggctgagccaggagagatgcagctggaattt
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Rat mRNA for protein tyrosine phosphatase, complete cds
D38072
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135. .1283
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
Method for examining ischemic conditions
Patent: WO 0188188-A 1063 22-NOV-2001;
School Juridical Person Nihon University (JP)
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634 c 681 g 745
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Search completed: May 26, 2002, 10:35:23 Job time: 12938 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 26, 2002, 10:42:10 ; Search time 56.14 Seconds (without alignments) 1184.429 Million cell updates/sec. Run on:

US-09-600-358A-4 3615 1 MDQREILQKFLDEAQSKKIT.....RPSKSVKLRSPKSGKNFSWL 692 Title: Perfect score: Sequence:

Scoring table:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SITMMARTES

	Description	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	leukocyte common a	HPTP beta-like tyr	protein-tyrosine-p	protein-tyrosine-p	leukocyte common a	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	probable protein-t		protein-tyrosine-p												
SUMMARIES	Ω	B44390	JC1368	S55345	ЭН0609	S48748	A46546	S68700	138670	A28334	TDRTLT	JC6312	S20825	B48148	JC5167	T43148	S17670	A48066	A46151	S17669	A48148	A54080	JN0805	A53593	A56178	A55651	D54689	C54689	m	A57068
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	Leukocyte antigen-	protein-tyrosine-p	leucocyte common a	leukocyte antigen-	protein-tyrosine-p	probable protein-t										
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	467.5	466.5	466.5	465	463.5	462.5	461	460	460	457.5	456.5	456	454.5	454.5	453	449
,	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1 B44390 Protein-tyrosine-phosphatase (EC 3.1.3.48) PEP, nonreceptor type 8 - mouse Protein-tyrosine-phosphatase PEP C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: B44390; S71952; S27876 R;Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L. Mol. Cell. Biol. 12, 2396-2405, 1992 A;Title: Characterization of hematopoietic intracellular protein tyrosine phosphatase
 , and threonine-rich sequences. A.Reference number: A44390, MVID:92236615 A.Accession: B44390 A.Molecule type: mRNA A.Residues: 1-802 < WAIT> A.Cross-references: GB:M0388; NID:9200522; PIDN:AAA39994.1; PID:9200523 R.Cloutier, J.F.; Veillette, A. EMBO J. 15, 4909-4918, 1996
 A;Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyro A;Reference number: S71952; MUID:97045099 A;Reference number: S71952 A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 495-789 <clo> C;Comment: This protein is found primarily in hematopoietic tissues.</clo>
Ajedne: 'Ozpep Gjornela: physically associates with inhibitory tyrosine protein kinase Csk; interac Gjenction: Albescription: probably an effector and/or regulator of tyrosine protein kinase csk i Gjenctamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-pho Gjency-production: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-pho Gjency-production: protein-tyrosine-phosphatase homology cPrP> Fj64-28/Domain: protein-tyrosine-phosphatase homology cPrP> Fj63-621/Region: proline-rich Fj613-621/Region: proline-rich Fj613-621/Region: proline-rich Fj613-621/Region: proline-rich Fj613-621/Region: proline-rich
 Courty Match Ouery Match Est Local Similarity 68.5%; Score 2356.5; DB 1; Length 802; Best Local Similarity 68.5%; Pred. No. 5.2e-139; Matches 474; Conservative 66; Mismatches 139; Indels 13; Gaps 6; Qy
 QY 61 KDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPRAYIATQGPLSTTLLDEWRMIWEY 120

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C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-ph C; Keywords: phosphorotein; phosphoric monoester hydrolase; tyrosine-specific phosphates F; $8-282/Domain: protein-tyrosine-phosphatase homology cPTP>. F; $213/Active site: Cys (phosphocysteine intermediate) #status predicted F; 237/Binding site: substrate phosphate (Arg) #status predicted
                                          A;Title: Chromosomal localization of the protein tyrosine phosphatase G1 gene and A;Reference number: S41746; MUID:94156037
                                                                                       A;Molecule type: mRNA
A;Residues: 59-127, YY,',130-134,'TE' <TA2>
A;Note: sequence shown is wild type
C;Comment: PEST sequences in this widely expressed protein suggest that it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVDSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNY----SLPYDSKHQIRNASNV 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V-----IRD--KHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQQRTK 346
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               Inazawa,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 EEILQPPEPHPVPPILIPSPPSAFPTVTTVWQDNDRYHPKPVLHMVSSEQHSADLNRNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHDNTS------PLFRTPLSFTNPLHSDDS----DSDERNSDGAVTQNKTNISTASAT
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                                                                                                                                                                                                                                                                                                                  32.0%; Score 1157; DB 1; Length 780; 37.0%; Pred. No. 2.7e-64; tive 112; Mismatches 237; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---C---SNSKP-----VNAAGRYFNSKVPITRTKS-----TPFELIQQRETK-
               ..
 A:Note: sequence has been revised in reference A47506
R:Takekawa, M.; Itoh, F.; Hinoda, Y.; Adachi, M.; Ariyama,
FEBS Lett. 339, 222-228, 1994
sequence has been revised in reference A47506
                                                                                                                                                                               A;Cross-references: GDB:136846; OMIM:600079
A;Map position: 7q11.23-7q11.23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-120,'I',122-321,'I',323-494,518-525,'FLLMRKDM' <YA2>
A;Note: sequence extracted from NCBI backbone (NCBIN:127945, NCBIP:127946)
                                                                                                                                                                                KHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQ---QRTKMEIKESSSFDF 357
 SVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNS
                                                                         LNQESAVLATAPRIDDEIPPPLPVRTPESFIVVEEAGEFSPNVPKSLSSAVKVKIGTSLE
              RTSEISAKEELVLHPAKSSTSFDFLELNYSFDKNADTTWKWQTKAFPIVGEPLQKHQSLD
                                                           ETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAI
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Qy 632 AGEFSPNVPKSLSSAVKVKIGTSLEWGGTSEPKKFDDSVILRPSKSVKLRSPKSG 686	OY 380 DFLELNYSFDKNADTTMKW
Qy 687 KNF 689	Oy 424 EGCSNSKPVNAAGRYFNSKVPITRTKSTPFELIQQRETKEV 464
Db 731 IHY 733	Db 457 RGHAIKIKSASSSVVDRT-SKPQELSAGALKVDDVSQNSCADCSAAHSHRAAE 508
RESULT 3 S55345	Qy 465 DSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNYSLPYDSK 507
protein-tyrosine-phosphatase (EC 3.1.3.48) PTP-PEST - mouse C; Species: Mus musculus (house mouse)	508 HQIRNASNYESSWPPSGTS
C; Date: 10-Oct-1995 #sequence_revision 01-Nov-1996 #text_change 22-Jun-1999 C; Accession: S55345; S54261; I48666	:: : :
K:Charest, A.; Wagner, J.; Shen, S.H.; Tremblay, M.L. Blochem. J. 308, 425-432, 1995 B.Title: Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyrosine n	Qy 548 SKMSLDLPEKQDGTVPPSSLLPTSSTSLFSYNSHSSLSLNSPTNISSLLNQESAV 603
•	613 SDGAVTRNKTSISTASAT-
A;Molecule Lype: LDNA A;Residues: 1-775 <cha> A;Cross-references: EMBL:X86781; NID:G804997; PIDN:CAA60477.1; PID:G804998</cha>	QY 604IMTAPRIDDEIPPLEVRYPESFITVE 630 : : : :
A;Description: Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyro A;Reference number: S54261	
	protein-tyrosine-phosphatase (EC 3.1.3.48) P19 - mouse N.Alternate names: protein-tyrosine-phosphatase PTPTY43 C.Spacies: Wis miscallis (Anisa maiss)
1804998	C.) Decress. mas missering Judges Mouse, C.) Date: 10-Sep-1999
	R;den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W. Riochem Biochew Res Commun 184 1241-1249 1992
otein-tyrosine-phosp	A;Title: Differential expression of a novel murine non-receptor protein tyrosine phos A;Reference number: JH0609; MUID:92272714
ted	A; Accession: JH0609 A; Molecule type: mRNA A; molecule type: mRNA
	A) RESIDUAS: 1-7/3 KUDN/ A)CTOSS: Teferences: GB:X63440; GB:S36169; NID:9416181; PIDN:CAA45037.1; PID:9416182 A:Experimental source: embryonic carcinoma cell. p19 cell
ore 1127.5; DB 2; Length 775; ed. No. 1.9e-62;	A; Accession: PS0365 A; Status: nucleic acid sequence not shown
ZOU; CUISELVALIVE 109; MISMACCHES 106; INDEIS 209; GAPS 26; MNORETIONETINENSKITTKREPANERIKIKENOCHWVRANKWARMENIK 66	A;Residens: 88-91, G',93-110, G',112-118,'S',120,'T',122 <de2></de2>
I	Ajaxper imperial source: embiyonic calcinoma cell, fis cell, cione firss Ajacession: F80369 Ajatus: nucleic acid sequence not shown
57 KNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPRAXIATQGPLSTTLLDFWRM 116	A:Molecule type: mRNA A.Residues: 88-91,'G',93-109,'LG',112-120,'T',122 <de3> A:Experimental source: embryonic carcinoma cell, P19 cell, clone PTP59</de3>
61 KNRYKDILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPFRNTVIDFWRM 120	A; Accession: PS0366 A; Status: nucleic acid sequence not shown
OY 11/ THEENVLITYMACMERGERYMACERYMACEGERYSUSCERRENDINTHTLKY 1/6 121 IWEXINVIIVMACREFEMGREKKCERYWPLYGEDPITFAPFKISCENEGARIDYFIRTLLL 180	A.Molecule type: mRNA A.Residues: 88-91, YRY',94-109, 'LA',112-118,'S',120-122 <de4> A.Experimental source: embryonic carcinoma cell, P19 cell, clone PTP42</de4>
Qy 177 KENSETRIIVQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICHHCSAGCGRTCV 236 : : : :	R;Yi, T.; Cleveland, J.L.; Ihle, J.N. Blood 78, 2222-2228, 1991 A;Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells
237 ICAIVDXTWMILKDGIIPENFSVFSIIREMPTORPSIVOTOBOXFIVYNAVIETERROMD 296	A; Actesion: G61180; MOLD: 92092002 A; Accession: G61180 with conceptual translation
1	A; Molecule type: mrNA A; Residues: 127, 17, 129-229 < YIAA A; Residues: 127, 17, 129-229 < YIAA A; Residues: 127, 17, 129-229 < YIAA A; Parameters: 127, 17, 17, 129-229 < YIAA A; Parameters: 127, 17, 129-229 < YIAA A; Parameters: 127, 17, 17, 17, 17, 17, 17, 17, 17, 17, 1
Qy 297 VIRDKHSCTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQQRTKME 348 1	C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-ph C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-ph C; Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phospha F; 55-299/Domain: phosphatase catalytic domain #status predicted <pcd></pcd>
349 IKESSSFDFRTSEISAKEELVLHPAKSSTSF 379	F;58-282/Domain: protein-tyrosine-phosphatase homology <ptp> F;231/Active site: Cys (phosphocysteine intermediate) *#status predicted F;237/Binding site: substrate phosphate (Arg) #status predicted</ptp>
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leukocyte common antigen long splice form precursor - human
N.Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; 7200 glycopro
N.Contains: leukocyte common antigen intermediate splice form; leukocyte common antig
C; Species: Homo saptens (man)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C; Date: 10-Sep-1999 #sequence change revision 10-Sep-1999 #text_change 21-Jan-2000
C; Date: 10-Sep-1999 #sequence change 21-Jan-2000
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F;58-282/Domain: protein-tyrosine-phosphatase homology <PTP>F;231/Active site: Cys (phosphocysteine intermediate) #status predicted F;237/Binding site: substrate phosphate (Arg) #status predicted
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R; Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
Bristol. 6, 1251-1257, 1987
A; Title: Structural variants of human T200 glycoprotein (le
A; Reference number: A91066; MUID:87275816
A; Accession: A29449
                                                                                                                                                                                                                                                                                                     89:
                                                                                                                                                                                                                       Score 1042; DB 1;
Pred. No. 1.4e-57;
                                                                                                                                                                                                                                                           ; Pred. No. 1.4e
62; Mismatches
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Best Local Similarity 53.5
Matches 201; Conservative
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S48748
R;Morlyama, T.; Kawanishi, S.; Inoue, T.; Imai, E.; Kaneko, T.; Xia, C.; Takenaka, M.; N
R;EBS Lett. 353, 305-308, 1994
A;Title: CDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kidne
A;Reference number: S48748; MUID:95046282
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A; Residues: 1-382 <MOR>
A; Residues: 1-382 <MOR>
A; Cross-references: GB:D38072; NID:9567262; PIDN:BAA07266.1; PID:9699627
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosp
C; Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
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Length 773;
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DB 1;
                                                                                      175;
                                         Pred. No. 5e-61;
                                                                                  Mismatches
    Score 1104.5;
                                                                                  Conservative 103;
30.6%;
35.6%;
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Gaps

Length 1238;

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S68700
HPTP beta-like tyrosine phosphatase precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68700
B;Kuramochi, S.; Matsuda, S.; Matsuda, Y.; Saitoh, T.; Ohsugi, M.; Yamamoto, T.
FEBS Lett. 378, 7-14, 1996
A;Title: Molecular cloning and characterization of Byp, a murine receptor-type tyrosi A;Reference number: S68700
A;Reference number: S68700
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1238 <KRNA
A;Residues: 1-1238 <KRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Map position: 2E1-2
C; Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III
C; Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III
C; Superfamily: phosphorotein
F; 1-28/Domain: signal sequence #status predicted <SIG>F; 29-1238/Product: HPTP beta-like tyrosine phosphatase #status predicted <MAT>F; 267-347/Domain: fibronectin type III repeat homology <3FR>F; 367-347/Domain: protein-tyrosine-phosphatase homology <PTP>F; 966-1188/Domain: protein-tyrosine-phosphatase homology <PTP>F; 140/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 1146/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: GB:D45212; NID:91208432; PIDN:BAA08146.1; PID:91208433 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 YDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLII 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       918 KSKLIRVENFEAYFKKQQADSNCGFAEEYEDLKLIGISLPKYTAEIAENRGKNRYNNVLP 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 QSKKITKEEFANEFLKLKRQST----KYKADK----TYPTTVAENAKNIKKNRYKDILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 VMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 TIYQFHYKNWPDHDVPSSIDPILELIWDVRCY--QEDDSVPICIHCSAGCGRTGVICAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL:U10886; NID:g558754; PID:g558755 A; Experimental source: HeLa cells R; Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, Blood 84, 4186-4194, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.2%; Score 513; DB 2; L
39.0%; Pred. No. 7.2e-24;
Live 50; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.2%
Best Local Similarity 39.0%
Matches 115; Conservative
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A; Residues: 1-1337 <RES>
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F;851/Active site: Cys (phosphocysteine intermediate) #status predicted
F;857/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                    A.Molecule type: mRNA
A.Residues: 32-192 <RA2>
A.Residues: 32-192 <RA2>
A.Residues: 32-192 <RA2>
A.Residues: 32-192 <RA2>
A.Stronli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A.Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative
A;Reference number: I57658; MUID:90066468
A;Accession: I57658
A;Molecule type: mRNA
A;Residues: 1-31,193-649,'L',651-869,'G',871-872,'A';874-1206,'P',1208-1304 <RAL>
A;Cross-references: GB:Y00062; NID:g34275; PIDN:CAA68269.1; PID:g34276
A;Experimental source: clones pHLC-1 and lambdaHLG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1020 FIMSYWKPEVMIAAQGPL-KETIGDFWOMIFORKVKVIVMLTELKHGDQEICAQ---YWG 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQYTNWSVEQLPAEPKEL 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLSTTLLDFWRMIWEYSVLIIVWACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 146-192 <RES>
A;Cross references: GB:M29253; NID:g187020; PIDN:AAA59497.1; PID:g553521
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE--FORLPSYRSWRTOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 DQREILQK------FLDEAQSKKITKE--EFANEFLKLKRQSTKYKADKTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|:|:|:::
EQQELVERDDEKQLMNVEPIHADILLETYKRKIADEGRPFLAEFQSIPRVFSK-----F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.2%; Score 514.5; DB 1; Length 1304; 28.2%; Pred. No. 6.3e-24; tive 86; Mismatches 241; Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:119768; OMIM:151460
A;Map position: 1q31-1q32
C;Superfamily: leukocyte common antigen; leukocyte common antigen
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----KHHKSTPLLIH 1166
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                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                 A; Status: not compared with conceptual translation
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                                                                                                                   A; Accession: B29449
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Best Local Simi
Matches 166;
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novel

A;Title: Molecular cloning, characterization, and chromosomal localization of a

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us-09-600-358a-4.rpr

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PTOTE, Natl. Meads Sci. U.S. N. 83, 6340-6344, 1886

PTOTE, Natl. Meads Sci. U.S. N. 83, 6340-6344, 1886

Ancleasion. A29818

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llarity 27.8%; Pred. No. 1.8e-23;
Conservative 84; Mismatches 237; Indels 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 174; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and C; Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repeat C; Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repeat S; 36-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <SIG. F; 36-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT> F; 206-283/Domain: fibronectin type III repeat homology <3FNA> F; 206-283/Domain: fibronectin type III repeat homology <3FNB> F; 355-445/Domain: fibronectin type III repeat homology <3FNB> F; 555-50/Domain: fibronectin type III repeat homology <3FNB> F; 555-50/Domain: fibronectin type III repeat homology <3FNB> F; 559-50/Domain: fibronectin type III repeat homology <3FNB> F; 559-50/Domain: fibronectin type III repeat homology <3FNB> F; 559-50/Domain: fibronectin type III repeat homology <3FNB> F; 568/Domain: transmembrane #status predicted <TNNS> F; 572-808/Domain: transmembrane #status predicted <TNNS F; 572-808/Domain: transmembrane #status predicted <TNNS F; 572-808/Domain: transmembrane #status predicted <TNNS 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse N;Alternate names: 200K leukocyte common antigen; CD45; PTPTY1; T-cell surface glycoprot N;Contains: protein-tyrosine-phosphatase (T-cell variant)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #Sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A28334; A29381; A61180; A60933; A33522; A29075; I54450
R;Thomas, M.L.; Reynolds, P.J.; Chain, A; Ben Neriah, Y.; Trowbridge, I.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
A;Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
A;Reference number: A28334; MUID:87260986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>
7:21,283,293,104,142,172,123,231,288,278,342,351,376,391,396,413,431,501,525,536,582,603,6
F;1239/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1245/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                   A; Residues: 1-216, 'LTGVRKAA', 225-260, 'G', 262-285, 'GTEGGLDASNTERSRA', 302, 'S', 304, 'TAPVHDBA; Cross-references: GB:D37781; NID:g633072; PIDN:BAA07035.1; PID:g633073
C;Comment: Enhanced expression of this protein with increasing cell density suggests a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLII 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 TIYQFHYKNWPDHDVPSSIDPILELIWDVRCY--QEDDSVPICIHCSAGCGRTGVICAIV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 VMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : : | | : : | | 1254 RLIYQIENENTV----DVYGIUYDERMHRPLAWQCTEDQYVFLNQCVLDIVRSQKD 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 508; DB 1; Length 13: 38.3%; Pred. No. 1.7e-23; Live 51; Mismatches 111; Indels
                     A;Reference number: 152599; MUID:95086212
A;Accession: 152599
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A28334
A; Molecule type: mRNA
A; Residues: 1-1291 <THO>
A;Coss-references: GB: M22455
R; Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
                                                                                                                                                                                                                                                                                                                                                              A,Gene: GDB:PTPRJ
A,Cross-references: GDB:385040; OMIM:600925
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 19q13.4-19q13.4
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Matches 113; Conservative
                                                                                                                                                     Molecule type: mRNA
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A; Atcoss Jour, 19409
A; Residues: Preliminary; translated from CB/EMBL/DDBJ
A; Rolecule type: mRNA
A; Residues: 1-30,163-180 cMCC>
A; Residues: 1-30,163-180 cMCC>
A; Cross-references: GB:840716; NID:9252015; PIDN:AAB22648.1; PID:9252016
A; Cross-references: GB:840716; NID:9252015; PIDN:AAB22648.1; PID:9252016
C; Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
C; Superfamily: Leukocyte common antigen; Jeycoprotein; phosphoprotein; phosphory F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-546/Domain: signal sequence #status predicted <SIG>
F; 24-546/Domain: extracellular #status predicted cSIG>
F; 24-30,122-1273/Product: leukocyte common antigen, splice form 2 #status predicted <F; 24-30, 1-21,163-218/Product: leukocyte common antigen, splice form 3 #status predicted <F; 24-30, 7-3121,163-218/Product: leukocyte common antigen, splice form 3 #status predicted <F; 24-30, 7-3121,163-218/Product: leukocyte common antigen, splice form 3 #status predicted <F; 24-30, 7-3121,163-218/Product: leukocyte common antigen cytosolic domain homology <LAC>
F; 56-1206/Domain: intracellular #status predicted <INT>
F; 66-1206/Domain: intracellular #status predicted <INT>
F; 66-1206/Domain: protein-tyrosine-phosphatase homology <PTP>
F; 64-870/Domain: protein-tyrosine-phosphatase homology stee: carbohydrate (Asn) F; 822/Active site: cys (phosphoryteteine intermediate) #status predicted
F; 828/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 1063/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 187-189, Kr, 191-192, Kr, 208-1273 <THO>
A; Residues: 187-189, Kr, 191-192, Kr, 208-1273 <THO>
A; Cross-references: GB: M10072; GB: M81859; NIDD: g205140; PIDN: AAA41513.1; PID: g205143
A; Note: the translation in GenBank entry RATLCA1, release 113.0, begins at non-intiti
A; Note: parts of this sequence were determined by protein sequencing
R; McCall, M.N.; Shotton, D.M.; Barclay, A.N.
Immunology 76, 310-317, 1992
A; Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy
A; Reference number: 154569; MUID: 92340120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the rat leukocyte-common antigen (T200) spans
                                                           A; Note: the sequence in GenBank entry, RATLCAIV, release 113.0, has the codon AGG for R; Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
Adv. Exp. Med. Biol. 237, 3-7, 1988
A; Title: The leukocyte-common antigen (L-CA) family.
A; Reference number: A60241; MUID:89319817
A; Accession: A60241
     GB:M25823; GB:M24611; NID:9205159; PIDN:AAA41521.1; PID:9205160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 30-161 <BARS>
R;Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
Cell 41, 83-93, 1985
A;Title: Evidence from cDNA clones that the rat leukocyte
A;Reference number: A02247; MUID:85201691
A;Accession: A02247
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
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A; Residues: 20-30,163-218 <BARI>
A; Residues: 20-30,163-218 <BARI>
A; Cross-references: GB:M25820; GB:M24611; NID:g205153; GB:Y00065; GB:K03039; GB:M10072;
A; Experimental source: splice form 1
A; Note: the translation in GenBank entry RATLCAI, PIDN:AAA41518.1, PID:g205154, release A; Accession: B29450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Species: Quantification or Second S
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A;Accession: D29450
A;Accession: D29450
A;Accession: D29450
A;Accestion: D29450
A;Accession: D29450
A;Ac
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A;Residues: 19-30,122-218 <BAR2>
A;Cross-references: GB:M2581; GB:M24611; NID:g205155; PIDN:AAA41519.1; PID:g205156;
A;Experimental source: splice form 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1092 ELRHSKRKEPRT------VYQY------QCTTWKGEELPAEPKDLVSMIQDLKQK- 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464
     RYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIW 118
                                                                                                                                                                                                            EYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKF 178
                                                                                                                                                                                                                                                                                                        729 EQKATVIVMVTRCEEGNRNKCAEYWPSMEEGTRAFKDIVVTINDHKRCPDYIIQKLNVAH 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 VICAIVDYTWMLLKDGIIPE-NFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLEL--FK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQMDVIRDKHSGTESQAKHCIPEKNHTLQADSYSPNLPK-STTKAAKMMNQQRTKMEIKE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSFDFRTSEISAKEELVL----HPAKSSTSFDFLELNYSFDKNADTTMKWQTKAFPIVG 407
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                                                                           179 NSET---RTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               904 ETEVNLSELHSCLHNMKKRDPPSDPSPLEAE--YQRLPSYRSWRTQHIGNQEENKKKNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 EPLOKHQSLDLGSLLFEGCSNSKP---VNAAGRYFNSKVPITRTKSTPFELIQQRETKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNYSL-PY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukocyte common antigen precursor, splice form 4 - rat
N;Alternate names: CD45; L-CA; Ly-5; T200
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A; Residues: 20-30,73-121,163-218 <BAR3>
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A Ancestion: 184031
A Molecule Page mRA
A Molecule Sequence extracted from GenBank
R: Plutaky J. 7: Neel, B. 6.7: Rosenberg, R.D.
Proc. Natl. Acad. Sci. U.S.A. 80, 1123-1127, 1992
Proc. Natl. Acad. Sci. U.S.A. 80, 1123-1127, 1992
Proc. Natl. Acad. Sci. U.S.A. 80, 1123-1127, 1992
A Molecule Pype: mRN
A Molecule Pype: mRN
A Molecule Pype: mRN
A Molecule Extracted from Norg backbone (NUBIN:79619, NOBIP:79620)
R: Shen. S. H: Bastlen, L.; Posner, B. I.; Chretien, P.
A) Title: corridendum: A protein-tyrosine phosphatase with sequence similarity to the NATILIE: corridendum: A protein-tyrosine phosphatase with sequence similarity to the NATILIE: corridendum: A protein-tyrosine phosphatase with sequence similarity to the NATILIE: corridendum: A protein-tyrosine phosphatase with sequence similarity to the NATILIE: corridentum: A protein-tyrosine phosphatase with sequence similarity to the NATILIE: corridentum: A protein-tyrosine phosphatase with sequence similarity to the SH2 domain of A MOLECULE Pype: mRNA
A MOLECUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 6 - human NiAlternate names: hematopoietic cell phosphatase HCP; protein-tyrosine-phosphatase 1 C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; State: 19-may-1994 #sequence_revision 08-Feb-1996 #text_change 11-Jun-1999
C; Accession: B42031; #sequence_revision 08-Feb-1996 #text_change 11-Jun-1999
C; Accession: B42031; A38189; S20825; S17234; S20837
Nol. Cell. Biol. 12, 836-846, 1992
A; Title: Protein tyrosine phosphatase containing SH2 domains: characterization, prefer A; Reference number: A42031; MUID:92123209
                                                                                                                                                                                                                                                                                                                                                               | : | | : | | | DLSQGCPQYWPEEGMLRYGPIQVECMSCSMDCDVINRIFRICNLTRPQEGYLMVQQFQYL 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1396 MVKRONVV-------DVFHAVKTLRNSKPNNVEAPEQYRFCYDVALEYLES 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 M-QAQKVMHVSSAELNYSLPYDSKHQIRNASNVKHHDSSALGVYSYIPLVENPYFSS 540
                                                                            1230 YINAALMDSYRQPAAF-----IVTQYPLPNTVKDFWRLVYDYGCTSIVMLNEV
                                                                                                                                                                                                                                                                                                                   436 GRYPNSKVPITRIKSTPFELI-----QQRETKEVDSKENFSYLESQPHDSCF-
                                                                                                                                                         389 DKNADTIMKWQIKAF----PIVGEPLQKHQSLDLGSLLFEGCSNSKPVNA---
    342 QQRTKM--EIKESSSFDFRTSEISAKEELVLHPAKSSTSFDFLELNYSF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SYWKPEMMIAAQG-----PLKETIGDFW 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMIFORKVKVIVMLTELMSGDQEVCAQYWGEGKQTYGDMEVMLKDTNKSSAYI-LRAFEL 1075
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                                                                                                                                                         339 MANQQRTKMEIKESSSFDFRTSEISAKEELVLHPAKSSTSFDFLELNYSFDKNADT--TM 396
                                                                                                                                                                                                      KWQTKAFPIVGEPLQKHQSLDLGSLLFEGCSNSKP---VNAAGRYFNSKVPITRTKSTPF 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELIQQRETKEV----SCFVEMQAQKV 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIR--TLKVKFNSETRTIYQFHYKNWPDHDV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKHSCTESQAKH-------CIPEKNHTLQ--ADSYSPN--LPKSTTKAAKMMN 341
282 LVYNAVLEL--FKRQMDVIRDKHSGTESQAKHCIPEKNHTLQADSYSPNLPK-STTKAAK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 123; Gaps
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                                                                    873 LIHOALVEYNOFGETEVNLSELHSCLQNLKKRDPPSDPSPLEAE--YQRLPSYRSWRTQH
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Pred. No. 2.3e-22;
.; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1076 RHSKRKEPRTVYQYQCTTWKGEELPAEPKDLVTLIQNIK 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- LNYSLPYDSKHQIRNASNVK 517
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Best Local Similarity 27.0%;
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Query Match 13.4%; Score 483.5; DB 2; Best Local Similarity 32.5%; Pred. No. 1.7e-22; Matches 123; Conservative 67; Mismatches 119;
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F;346-434/Domain: fibronectin type III repeat homology <3FR>
F;346-434/Domain: protein-tyrosine-phosphatase homology <PTP>
F;811-1105/Domain: protein-tyrosine-phosphatase homology <PTP>
F;1172-1396/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1057/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1063/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: B48148
R; Barnea, G.; Silvennoinen, O.; Shaanan, B.; Honegger, A.M.; Canoll, P.D.; D'Eustachio, Mol. Cell. Biol. 13, 1497-1506, 1993
A; Title: Identification of a carbonic anhydrase-like domain in the extracellular region A; Reference number: A48148; MUID:93180796
A; Accession: B48148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: protein-tyrosine-phosphatase, receptor type gamma; carbonic anhydrase hom
ne-phosphatase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma precursor - mouse C;Species: Mus musculus (house mouse) C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
                                             14;
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KKKLEVLQSQ-KGQESEYGNI------TYPPAMKNAHAKASRTSSKHKEDVYENL 567
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                                             Gaps
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A;Residues: 1-1442 <BAR>
A;Cross-references: GB:L09562; NID:g293773; PIDN:AAA40022.1; PID:g293774
                                                                                                                                                                                                                                                                        OSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELS
                                                                                                                                                                                                                                                   CMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSE-TRTI
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                                             62;
      Length 595;
    ; Score 485; DB 1;
; Pred. No. 1.4e-22;
69; Mismatches 129
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13.4%;
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A Note: extensively polymorphic
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  Query Match
Best Local S
Matches 128
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A. Cocession: JC5167
A. Accession: JC5167
A. Residues: I-593 < PAR>
A. Residues: I-593 < PAR>
A. Residues: I-593 < PAR>
A. Cross = references: GB:1036620; NID:g1054939; PIDN:AAC60049.1; PID:g1054940
C. Comment: This enzyme plays positive roles in mitogenic signaling and early developm C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phoc; Selvands: phosphoric monoester hydrolase; tyrosine-specific phospha F: 6-105.112-193/Domain: SH2 ** status** predicted <SH2>
F: 6-100/Domain: SH2 homology <SH2A>
F: 112-214/Domain: SH2 homology <SH2A
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Gene 177, 93-97, 1996
A; Title: Cloning and expression of the chicken protein tyrosine phosphatase SH-PTP2.
A; Reference number: JC5167; MUID:97080506
                                                                                                                                                                                                                                                        946 MITNLVEKGRRKCDOYW--PTENTEEYGNIIVTLKSTKVHACYTVRRLSVRNTKVKKGOK 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - chicken NiAlternate names: phosphotyrosine phosphatase; PTP1D; PTP2c; SH-PTP2; SyP C; Species: Gallus gallus (chicken C; Species: Gallus gallus (chicken C; Species: 21-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1253 AEDEFVYWPSREES---MNCEAFTVTLISKDRLCLS------NEGIIIHDFILEA 1299
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F;559-570/Region: proline-rich
F;459/Active site: Cys (phosphocysteine intermediate) #status predicted
TGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKR
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14;

Gaps

69

Length 593; Indels

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Search completed: Nob time: 5812 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                            probable protein-tyrosine-phosphatase (EC 3.1.3.48) - horn shark
N.Alternate names: CD45 homolog
N.Alternate names: CD45 homolog
N.Alternate names: CD45 homolog
S.Species: Heterodontus francisci (horn shark)
C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C.Accession: T43148
R.McMuara, M.; Mattheway, R.J.; Robb, B.; Bork, P.; Thomas, M.L.
Submitted to the EMBL Data Library, August 1995
A.Reference number: Z22317
A.Accession: T43148
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-1200 < OKD.
A.Cross-references: EMBL:U34750; NID:g1304393; PID:g1335805; PIDN:AAB01087.1
C.Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
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                                                                                                            SVLIIVMACMEYEMGKKKCERYWAEPGEMQL-EFGPFSVSCEAEKRKSDYIIRTLKV--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WRMIWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRT 173
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DQREIL-----QKFLDEAQSKKITKEE-FANEFLKLKRQSTKYKADKTYPTTVAENAK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKVKFNSE---TRIIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGRTGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLEL
AQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVEL
                                                     SLITSDED-----SSYINANFIKGVY------GPKAYIATQGPLSTTLLDFWRMIWEY
                                                                                                                                                                                                                          TGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAV---LEL
                                                                                                                                                                                                                                                                              FKRQMD-------VIRDKHSGTESQAKHCIPEKNHTLQADSYSPNLPKST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 483.5; DB 2; Length 1200; 24.2%; Pred. No. 4.7e-22;
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574 EDSARVYENVGLMQQQKS 591
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May 26, 2002, 12:19:02

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452
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FKRQMDVIRDKHSGTESQAKHCI-----PEKNHTLQADSYSPNLPKST---TKAAKMM 340
                                             Y-----EYGETEVSLSELPKHLINFKKNDPPSEPSMLEGE--FQRIPPYTDWRTQTTGRR
                                                                                                                                                                                             401 KAFPIVGEPLQKHQSLDLGSLLFEGCSNSKPVNAA--GRYFNS-----KVPITRTKSTP
                                                                                                                                                                                                                         FELIQQRETKEV-----DSKENFSYLE--SQPHDSCFVEM-----QAQKVMHVSSAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- IVVEEAGEFSPNVPKSLSSAVKVKIGTSLEWGGTSEPK
                                                                                                                         864 GENQSKNRSLSVIAYDYNRVTIKLEDE----KSKDSTS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPPLPVRTPESF---
291
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

 protein search, using sw model OM protein May 26, 2002, 12:17:55 ; Search time 39.31 Seconds Run on:

(without alignments)
681.606 Million cell updates/sec

US-09-600-358A-4 3615 1 MDQREILQKFLDEAQSKKIT.....RPSKSVKLRSPKSGKNFSWL Perfect score:

692

BLOSUM62 Scoring table: Sequence:

105224 segs, 38719550 residues Gapop 10.0 , Gapext 0.5 Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 08

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OTT T COUNTY

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SUMMARIES	ID	PTN8_MOUSE	PTNC_HUMAN	PINC_MOUSE	CD45_HUMAN	PTPJ_MOUSE	PTPJ_HUMAN	CD45_MOUSE	CD45_RAT	PTPK_HUMAN	PTN6_HUMAN	PTPG_MOUSE	PTPM_MOUSE	PTPZ_RAT	PTPK_MOUSE	PTPZ_HUMAN	PTPM_HUMAN	PTPG_HUMAN	PTNB_RAT	PTNB_HUMAN	PTPD_HUMAN	PTN6_MOUSE	PTPF_HUMAN	PTNB_MOUSE	PTP1_DICDI	PTP9_DROME	PTRA_HUMAN	PTRA_MOUSE	PTPG_CHICK	PTPO_MOUSE	PTP6_DROME	PTRA_RAT	LAR_DROME	PTN1_CHICK
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	Score	2356.5	1157	1130.5	516.5	513	208	499	493	492.5	485	485	479		478.5	478	7	47	473.5	473	471	468	467.5	466.5	463.5	462.5	460	460	456	452	446.5	441	439.5	436.5
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Q60673 mus musculu P49445 rattus norv	P35992 drosophila P56722 bos taurus	Q63259 rattus norv O16849 homo sanjen	P20417 rattus norv	P18031 homo sapien	P29074 homo sapien P29074 homo sapien	P35236 homo sapien
PTPN_MOUSE PTN7_RAT	PTP1_DROME PTPN_BOVIN	PTPN_RAT	PTN1_RAT	PTN1_HUMAN	PINS_HUMAN	PTN7_HUMAN
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979 359	1630 979	983	432	435	913	360
12.1	12.0 12.0	12.0	11.9	8.61	11.8	11.8
436	434	433	430.5	427.5	427	426.5
34 35	36 37	38 30 80	40	42	44	42

ALIGNMENTS

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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MATCHAWS R.J., Bowne D.B., Flores E., Thomas M.L.;
MATCHAWS R.J., Bowne D.B., Flores E., Thomas M.L.;
MATCHARACTERIZATION Of hematopoletic intracellular protein tyrosine
Thosphatases: description of a phosphatase containing an SH2 domain
and another enriched in proline-, glutamic acid-, serine-, and
threonine-rich sequences."

I. Mol. Cell. Biol. 12:2396-2405(1992).

I. Mol. Cell. Biol. 12:2396-2405(1992).

I. OTALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.

I. SUBCELLULAR LOCATION: Cytoplasmic.

I. SUBCELLULAR LOCATION: Cytoplasmic.

I. SUBCELLULAR LOCATION: SPLEEN, THYMUS, LYMPH NODE, AND BONE MARROW.

TYROSINE PHOSPHATASE FAMILY.
                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hematopoietic cell protein-tyrosine phosphatase 702-PEP (EC 3.1.3.48).
                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN-TYROSINE PHOSPHATASE.
BY SIMILARITY.
0F1E45339BD4613E CRC64;
                                     802 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, Q06124; ZSHP.
MGD; MG1107170; Ptpn8.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_prof__phphtase.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00194; PTPC; 1.
                                     PRT;
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                                     STANDARD;
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227 2
802 AA;
                                     PTN8_MOUSE
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ACT_SITE
SEQUENCE
RESULT 1
PTN8_MOUSE
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Query Match

65.2%; Score 2356.5; DB 1; Length 802;

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                                                         KDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTILLDFWRMIWEY 120
                                                                                          SVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNS 180
                                                                                                                                                                                                                                                             LGSLLFEGCSNSKPVNAAGRYFNSKVPITRTKSTPFELIQQRETKEVDSKENFSYLESQP 477
                        9
                                        9
         Gaps
                                                                                                                                                                    MEDLINE-9311215; PubMed-1472029; MEDLINE-93112015; PubMed-1472029; Takekawa M., Itoh F., Hinoda Y., Arimura Y., Toyota M., Sekiya M., Adachi M., Imai K., Yachi A.; "Cloning and characterization of a human cDNA encoding a novel
                                                                                                                           ETRT1YQFHYKNWPDHDVPSSIDP1LEL1WDVRCYQEDDSVP1C1HCSAGCGRTGV1CA1
                                                                                                                                                           VDYTWMLLKDG1IPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRD
                                                                                                                                                                                                                                                                                               HDSCFV-EMQAQKVMHVSSAELNYSLPYDSKHQIRNASNVKHHDSSALGVYSYIPLVENP
                                                                                                                                                                                                                                                                                                                               YFSSWPPSGTSSKMSLDLPEKQDGTVFPSSLLPTSSTSLFSYYNSHSSLSLNSPTNISSL
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                                 KHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQ----QRTKMEIKESSSFDF
                                                                                                                                                                                                                             RTSEISAKEELVLHPAKSSTSFDFLELNYSFDKNADTTMKWQTKAFPIVGEPLQKHQSLD
                         MDQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PINC_HUMAN STANDARD; PRT; 780 AA.
005209; Q16130;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Protein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)
         13;
         Indels
        66; Mismatches 139;
No. 1.5e-137
                                                                                                                                                                                                                                                                                                                                                                                                         WGGTSEPKKFDDSVILRPSKSVKLRSPKSGKN 688
Pred.
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
68.58;
        474; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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FEBS Lett. 339:222-228(1994).
-i- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94156037; PubMed-7509295;
Takekawa M., Itoh F., Hinoda Y., Adachi M., Ariyama T., Inazawa J.,
Imai K., Yachi A.;
"Chromosomal localization of the protein tyrosine phosphatase G1 ger
and characterization of the aberrant transcripts in human colon
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--- SUBCELLULAR LOCATION: Cytoplasmic.
--- DISEASE: DEFECTS IN PTPN12 ARE FOUND IN SOME COLON CANCERS.
--- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
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K -> R (IN COLON CANCER).

/FIId=VAR_006385.

V -> I (IN REF. 2).

V -> I (IN REF. 2).

N -> I (IN REF. 2).
                                                                                                                                                                                                                                                                        novel, human,
putative cytoplasmic protein-tyrosine-phosphatase.";
Biochem. Biophys. Res. Commun. 189:1223-1230(1992).
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llarity 37.0%; Pred. No. 8e-64;
Conservative 112; Mismatches 2:
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InterProj IPR000242; Tyr_prot_phphtase.
Pfam. PF001012; Y_phosphatase; 1.
PRINTS: PR00700; PRTYPHPHASE.
SMART; SM00194; PTPC; 1.
PR05ITE; PS001839; TYR_PHOSPHATASE_1; 1.
PROSITE; PS001839; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-93203262; PubMed-8454633;
Yang Q.C., Tonks N.K., Sommercorn J.;
"Cloning and expression of PTP-PEST. ?
                                                                                                                                                                                                                                                                                                                       protein tyrosine phosphatase.";
J. Biol. Chem. 268:6622-6628(1993).
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EMBL; M93425; AAA36529.1; --
EMBL; S69184; AAB30047.2; --
PIR; JC1368; JC1368.
HSSP; Q06124; ZSHP.
MIM; 600079; --
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                                                                                          297 V-----IRD--KHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQQRTK 346
                                                                                                                  300 LYEIHGAQKIADGVNEINTENMVSSIEPEKQ-----DSPPPKPPRTRS----CLVEGDAK 350
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30-MAY-2000 (Rel. 39, Last annotation update)
Protein-tyrosine phosphatase P19 (EC 3.1.3.48) (P19-PTP) (MPTP-PEST).
KFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                            411 KSTELPGKNESTIEQIDKKLERNLSFEIKKVPLQEGP----KSFDGNTLLNRGHAIKIKS
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MEDLINE-22272714; Pubmed-1590786;
den Hertog J., Pals C.E., Jonk L.J., Kruijer W.;
"Differential expression of a novel murine non-receptor protein tyrosine phosphatase during differentiation of P19 embryonal
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MEDLINE=93112015; PubMed=1472029;
Takekawa M., Itoh F...Hinoda Y., Arimura Y., Toyota M., Sekiya Adachi M., Imai K., Yachi A.;
"Cloning and characterization of a human cDNA encoding a novel putative cytoplasmic protein-tyrosine-phosphatase.";
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01-FEB-1996 (Rel. 33, Last seq
30-MAY-2000 (Rel. 39, Last anno
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                                                                                                                                                                                                                                                                                                    tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.3%; Score 1130.5; DB 1; Length 775; llarity 36.6%; Pred. No. 3.4e-62; Conservative 110; Mismatches 165; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
K -> N (IN REF. 1).
KQDSP -> DETS (IN REF. 1).
W -> V (IN REF. 1).
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                                                                                                                                                Charest A., Wagner J., Shen S.H., Tremblay M.L.; "Murine protein tyrosine phosphatase-PEST, a stable tyrosine phosphatase.";
Commun. 189:1223-1230(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD: MGII04673; Ptpn12.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_phosphatase.
InterPro; IPR000242; TYL_Pro; IPP01022.
PRINTS; PR00102; Y_phosphatase: 1.
PRINTS; PR00194; PTPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
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                                                                                      STRAIN-BALB/C;
MEDLINE-95289971; PubMed=7772023;
                                                                                                                                                                                                                                                                                                                                                                                                     TYROSINE PHOSPHATASE FAMILY.
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Q06124; 2SHP.
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Biophys. Res.
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les 280; Conserv
                                                             SEQUENCE FROM N.A.
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ALTERNATIVE SPLICING.
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01-AUG-1988 (Rel. 08, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)
                                                                                                                                                                                                                                                                                                                                                                     547
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                                                                                          DFLELNYSFDKNADTTMKW------QTKAFPIVGEPLQK-HQSLDLGSLLF 423
                                                                                                                                                  ---DLNRSYDKSAD----OWGKSESAIEHIDKKLERNLSFEIKKVPLQEGPKSFDGNTLLN 456
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MEDLINE-88061067; PubMed-2824653;
Streull M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
"Differential usage of three exons generates at least five different mRNAs encoding human leukocyte common antigens.";
J. Exp. Med. 166:1548-1566(1987).
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MEDLINE-90316033; PubMed-1695146;
MEDLINE-90316031; PubMed-1695146;
Strouli M., Krueger N.X., Thai T., Tang M., Salto H.;
"Distinct functional roles of the two intracellular phosphatase like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains of the receptor-linked protein tyrosine phosphatases LCA and LAR.";
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                                                                                                                                                                                                                                                  | :: : : | : : | : : | : RG--HAIKIKSA-----SSSVVDRT-SKPQELSAGALKVDDVSQNSCADCSAAHSHRAAE
                                                                                                                                                                                                                                                                                                                                   DSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNYSL-------PYDSK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.; "The leukocyte common antigen (CD45): a putative receptor-linked protein tyrosine phosphatase."; Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
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SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS ARE PRODUCED BY
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01-AUG-1988 (Rel.
16-OCT-2001 (Rel.
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P08575;
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PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
Glycoprotein; Transmembrane; Phosphorylation; B-cell; T-cell; Repeat; Alternative splicing; Hydrolase; Signal.
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EQQELVERDDEKQLMNVEPIHADILLETYKRKIADEGRPFLAEFQSIPRVFSK-----F 665
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GlycoSuiteDB; P08575; -.
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15 QSKKITKEEFANEFLKLKRQST----KYKADK----TYPTTVAENAKNIKKNRYKDILP 65
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Best Local Similarity
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PIKEARKPFNQNKNRYVDILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQG 725
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064455;
01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
PTPRJ OR BYP.
                                                                                                          PLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEK
                                     PRDETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGTRAFGDVVVKINQHK
                                                         RKSDYIIRTLKV---KFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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MEDLINE-96140699; PubMed-8549806;
Kuramochi S., Matsuda S., Matsuda Y., Saitoh T., Ohsugi M.,
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MCD, MGI-104574; PUPT].

MCD, MGI-104574; PUPT].

R InterPro; IPR0003961; FN_III.

R InterPro; IPR0003961; FN_LIII.

R InterPro; IPR000342; TYL_bhosphatase.

R Ffam; PF00041; fin3; 6.

R Ffam; PF000102; Yphosphatase; 1.

R RNNTS; PR00700; PRTYPHPHTASE.

R SMART; SM00104; PTPC; 1.

R SMART; SM00104; PTPC; 1.

R R SMART; SM00114; PTPC; 1.

R PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

R SIGNAL; 1.

R SIGNAL; PTPC; 1.

R POTENTIAL.
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FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
PROTEIN-TYROSINE PHOSPHATASE.
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FIBRONECTIN TYPE-III 3.
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7;

Gaps

20;

Mismatches 110; Indels

Score 513; DB 1; Pred. No. 5.9e-24;

14.2%; Sc. 39.0%; Pred 50; }

Conservative

Length 1238;

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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@18b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILINE-95086212; PubMed-7994032;
HONDA H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
Molecular cloning, characterization, and chromosomal localization of
a novel protein-tyrosine phosphatase, HPTP eta.";
Blood 84:4186-4194(1994).
-i- FUNCTION: MAY CONTRIBUTE TO THE MECHANISM OF CONTACT INHIBITION OF
                                          VMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSETR 183
                               YDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLII 125
                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Profean-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
(HPTP eta) (Density enhanced phosphatase-1) (DEP-1) (CD148 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95024024; Pubmed-7937872;
Oestman A., Yang Q., Tonks N.K.;
"Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
                                                                                                                              184 TIYQFHYKNWPDHDVPSSIDPILELIWDVRCY--QEDDSVPICIHCSAGCGRTGVICAIV
                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                       242 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is enhanced with increasing cell density.";
Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
                                                                                                                                                                                                                                       PRT; 1337 AA
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                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                      PTPJ_HUMAN STANDARD
012913; 015255;
01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
01-MAR-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P18052; 1YFO.
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PTPJ_HUMAN
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R InterPro; IPR000242; Tyr_prot_phphtase.

R Pfam; PF00102; Y_phosphatase; 1.

R PRINTS; PR00700; PRTYPHPHTASE.

SMART; SM00060; FN3; 6.

R SMART; SM00194; PFPc; 1.

R PROSITE; PS50056; TYR_PHOSPHATASE_1; 1.

R PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

R PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

R PSOSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.

R Signal; Glycoprotein; Transmembrane; Repeat; Hydrolase.

SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN-TYROSINE PHOSPHATASE
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14.1%; Score 508; DB 1; Length 13
Best Local Similarity 38.3%; Pred. No. 1.3e-23;
Matches 113; Conservative 51; Mismatches 111; Indels
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W; E686DE6D1F64236E CRC64;
                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
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InterPro; IPR003961; FN_III. InterPro; IPR000387; TYR_phosphatase.

MIM; 600925;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DEVELOPMENTAL STRAGE: EXPRESSION IS RESTRICTED TO THE HEMATOPOIETIC COMPARTMENT OF DEVELOPMENT.
-!- FTM. HEAVILY N- AND O-GLYCOSYLATED.
-!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                 126 VMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSETR 183
                                                      184 TIYQFHYKNWPDHDVPSSIDPILELIWDVRCY--QEDDSVPICIHCSAGCGRTGVICAIV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

tyrosine + phosphate.

SUBCELLULIAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCES: A NUMBER OF ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (Lymphocyte common antigen Ly-5) (CD45) (T200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raschke W.C.; "Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lymphocyte lineages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
-1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN
RECEPTOR. THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE
THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86313686; PubMed-2944116;
Saga Y., Tung J.-S., Shen R.-W., Boyse E.A.;
"Sequences of Ly-5 cDMs: isoform-related diversity of Ly-5 mRNA.";
Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                           242 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen F.-W., Saga Y., Litman G., Freeman G., Tung J.-S., Cantor Boyse E.A.; "Cloning of Ly-5 cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
                                                                                                                                                                                                               PRT; 1152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86042665; PubMed-3864163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 822-1152 FROM N.A. MEDLINE-87092355; PubMed-2948186;
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 10-124 FROM N.A.
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                              PTPRC OR LY-5
                                                                                                                                                                                                             CD45_MOUSE
P06800;
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PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
Glycoprotein; Transmembrane; Phosphorylation; B-cell; T-cell; Repeat;
Alternative splicing; Hydrolase; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 EYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     590 EQKATVIVMVTRCEEGNRNKCAEYWPSMEEGTRAFKDIVVTINDHKRCPDYIIQKLNVAH 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 VICAIVDYTWMLLKDGIIPE-NFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLEL--FK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDQREILQKFLDEAQSKKITKEE--FANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSET----RTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
FIRRONECTIN TYPE-III 1
FIRRONECTIN TYPE-III 1.
FIRRONECTIN TYPE-III 1.
PROTEIN-TYROSINE PHOSPHATASE 1.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIN-LINKED (GLCNAC...) (POTENTIN-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.8%; Score 499; DB 1; Length 1152; 27.6%; Pred. No. 3.8e-23; tive 83; Mismatches 239; Indels 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEUKOCYTE COMMON ANTIGEN.
EXTRACELLULAR (POTENTIAL)
email to license@isb-sib.ch).
                                                                                                                                      PIR; A29381; A29381.
HSSP; P18052; 1YFO.
MGD; MGI:97810; Ptprc.
InterPro; IPR0003961; FN_III.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
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                                                                                                                                                                                                                                                                                                                   Pfam; PF00041; fn3; 3.
Pfam; PF00102; Y_phosphatase;
PRINTS; PR00700; PRTYPHPHTASE.
                                          EMBL; M14342; AAA39458.1; -.
EMBL; M11934; AAA39461.1; -.
EMRT: M15174; AAA40161.1; -.
                                                                                  EMBL; M11934; AAA39461.1;
EMBL; M15174; AAA40161.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 27.6
Matches 173; Conservative
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SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                                                                 EMBL; Y00065; CAA68272.1; -.
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nes 158; Conservative
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11354
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                                                                                                                                                                               PIR; A60241; TDRTLT.
HSSP; P18052; 1YFO.
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Best Local Si
Matches 158,
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DOMAIN
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
  tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: THERE ARE DIFFERENT VARIANTS OF L-CA, WHICH ARISE BY ALTERNATIVE SPLICTING.
TISSUE SPECIFICITY: VARIANTS 4 AND 3 ARE FOUND IN THE LYMPH NODE, PARIANTS I AND 2 ARE FOUND IN THROCYTE AND LYMPH NODE.
PTH: HEAVILY N- AND O-GICCOSYLATED
PTH: HEAVILY N- AND O-GICCOSYLATED
PTH: THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION
ETQVNLSELHSCLHNMKKRDPPSDPSPREAE--YQRLPSYRSWRTQHIGNGGENKKKRRN 822
                                                 872
                              407
                                                                    464
                                                                                                             504
                                                                                                                                                                ELRHSKRKEPRT-----VYQY-----QCTTWKGEELPAEPKDLVSMIQDLKQK-995
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIRST ONE. CATAVITY: Protein tyrosine phosphate + H(2)0 = protein
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                              SSSFDFRTSE1SAKEELVL----HPAKSSTSFDFLELNYSFDKNADTTMKWQTKAFP1VG
                                                                    EPLOKHOSLDLGSLLFEGCSNSKP---VNAAGRYFNSKVPITRTKSTPFELIQQRETKEV
                                                                                        ------BIKETIGDFWQMIFQRKVKVI
                                                                                                             ------DSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNYSL-PY
                                                                                                                          VMLTELVNGDQEVCAQYWGEGKQTYGDME-----VEM---KDTNRASA---YLLRTF
                                                                                                                                                  DSKHQIRNASNVKHHDSSALGVYSYIPLVENPYFSSWP----PSGTSSKMSL--DLPEKQ
                                                SNVVPYDFNRVPLKHELEMSKESEPESDESSDD-----DSDSEETSKYINASFVM--
                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leukocyte common antigen variant 4 precursor (EC 3.1.3.48) (L-CA)
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 190-1255 FROM N.A.
MEDLINE-85201691; PubMed-3158393;
Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;
Fyidence from cDNA clones that the rat leukocyte-common antigen (T200) spans the lipid bilayer and contains a cytoplasmic domain 80,000 Mr.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SITES. SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                   Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.; Submitted (MAY-1987) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                              1255 AA
                                                                                                                                                                                                           -----LPKASPEGMKYH-KHASI 1012
                                                                                                                                                                                         559 DGTVFPSSLLPTSSTSLFSYYNSHSSL 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE SPLICING.
MEDLINE-87275817; PubMed-2440674;
                                                                                                                                                                                                                                                                                01-NOV-1986 (Rel. 03, Created)
01-AUG-1988 (Rel. 08, Last seq
                                                                                                                                                                                                                                                                                                                       (CD45) (T200) (Fragment).
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 41:83-93(1985).
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       MCBI_TaxID-10116;
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P04157;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B-cell; T-cell; Repeat;
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(POTENTIAL).
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(POTENTIAL).
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Pred. No. 1e-22;
89; Mismatches 222; Indels 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEUKOCYTE COMMON ANTIGEN VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHATASE
PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C257CBD2A355BCEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
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                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003961; FN_III.
Interpro; IPR003961; TYR_phosphatase.
Interpro; IPR000387; TYR_phosphatase.
Pfam; PF00011; fn3; 2.
Pfam; PF00102; Y_phosphatase; 2.
SMART; SM00060; FN3; 2.
SMART; SM00134; PTPC; 2.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
Glycoprotein; Transmembrane; Phosphorylation; B-callegative splicing; Hydrolase; Signal.
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                                                                                                                                                                                                EMBL; Y00065; CAA68273.1; EMBL; Y00065; CAA68274.1; EMBL; Y00065; CAA68275.1; EMBL; M25820; AAA41518.1; EMBL; M25822; AAA41520.1; EMBL; M25822; AAA41520.1; EMBL; M25823; AAA41521.1;
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                                                                                                                                                                                                                                 MMNQRTKMEIKESSSFDFRTSEISAKEELVLHPAKSSTSFDFLELNYSFDKNADT---TM 396
                                                                                                                                                                                                                                                                         397 KWQTKAFPIVGEPLQKHQSLDLGSLLFEGCSNSKP---VNAAGRYFNSKVPITRTKSTPF 453
                                                                                                                                                                                                                                                                                                                  ELIQQRETKEV----SCFVEMQAQKV 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96279245; PubMed-8663237;
Fuchs M., Mueller T., Lerch M., Ullrich A.;
"Association of human protein-tyrosine phosphatase kappa with members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I-FUNCTION: REGULÁTION OF PROCESSES INVOLVING CELL CONTACT AND ADHESION SUCH AS GROWTH CONTROL, TUMOR INVASION, AND METASTASIS. FORMS COMPLEXES WITH BETA-CATENIN AND GAMMA-CATENIN/PLAKOGLOBIN.
                                                                               :|:|::::
EQQELVERDEEKQLINVDPIHSDLLLETYKRKIADEGRLFLAEFQSIPRVFSK-----F
                           PTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYLATQG
                                       619 PIKDARKSQNQNKNRYVDILPYDYNRVELSEINGDAGSTYINASYIDGFKEPRKYIAAQG
                                                                 105 PLSTILLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEK
                                                                                                          RKSDYIIRTLKVKFNSET - - - RTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSV
                                                                                                                                                  PICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYE
                                                                                                                                                                                                       KYINASFVM-------PLKETIGDFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein-tyrosine phosphatase kappa precursor (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang Y., Gil M.C., Choi E.Y., Park S.H., Pyun K.H., Ha H.; "Molecular cloning and chromosomal localization of a human gene homologous to the murine R-PTP-kappa, a receptor-type protein
                                                                                                                                                                                                                                                                                                                                                                         1058 RHSKRKEPRIVYQYQCTTWKGEELPAEPKDLVILIQNIK 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                               1439 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the armadillo family.";
Biol. Chem. 271:16712-16719(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                            PTPK_HUMAN STANDARD; F
015262; 014763;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphatase.";
Gene 186:77-82(1997).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@license.).
                                                                                                                                      ΝI
BETA-CATENIN MAY BE A SUBSTRATE FOR THE CATALYTIC ACTIVITY OF PTP-
                                                                                                                               -!- TISSUE SPECIFICITY: HIGH LEVELS IN LUNG, BRAIN AND COLON; LESS IN LIVER, PARCREAS, STOMACH, KIDNEY, PLACENTA AND MAMARY CARCINOMA.

--- PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING.

--- SIMILARITY: CONTAINS 1 MAM DOMAIN.

--- SIMILARITY: CONTAINS 1 IMMONGCIOBULIN-LIKE C2-TYPE DOMAIN.

--- SIMILARITY: CONTAINS 4 FIRECNECTIN TYPE III-LIKE DOMAINS.

--- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHAFASE DOMAINS.
                                              CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 - protein
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EXTRACELLULAR (POTENTIAL).
                                                                    tyrosine + phosphate.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN; AT ADHERENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0014; PENTYPEILI.

REINTS; PRO00100; PRYTYPEILI.

REINTS; PRO00100; PRYTYPHHTASE.

REINTS; PRO00100; PRYTYPHHTASE.

REART; SM00100; PRYTYPHHTASE.

REART; SM00117; MAM; 1.

REART; SM00114; PTPC; 2.

REOSITE; PS50056; TYR_PHOSPHATASE_1; 2.

REOSITE; PS50056; TYR_PHOSPHATASE_1; 2.

REOSITE; PS500740; MAM_1; 1.

REOSITE; PS500700; MAM_2; 1.

REOSITE; PS50006; MAM_2; 1.

REOSITE; PS50006; MAM_2; 1.

REOSITE; PS50006; MAM_2; 1.

REOSITE; PS50006; MAM_2; 1.
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PROTEIN-TYROSINE PHOSPHATASE
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CLEAVAGE SITE (PROBABLE).
N-LINKED (GLCNAC...) (PO
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
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InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00041; fn3; 2.
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InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnII_repeat.
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Pfam; PF00102; Y_phosphatase;
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384
474
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InterPro; IPR000998;
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SIGNAL
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TRANSMEM
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   16;
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PYHATGLLSFIRRVKLSNPPSAGPIVVHCSAGAGRIGCYIVIDIMLDMAEREGVV----D 1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYWPDDTEV---YGDFKVTCVEMEPLAEYVVRTFTLERRGYNEIREVKQFHFTGWPDHGV 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.48) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Hematopoietic cell protein-tyrosine phosphatase) (SH-PTP1) (Protein-tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                 DSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVWACMEYEMGKKKCE 140
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Catarrhini; Hominidae; Homo.
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29.1%; Pred. No. 1.3e-2...
.... 77; Mismatches 167;
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(Rel. 24, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                       Matches 136; Conservative
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SIMILARITY: BELONGS TO THE NON-PECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. SUBCLASS THAT CONTAINS SH2 DOMAINS.
SIMILARITY: CONTAINS 2 SH2 DOMAINS.
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MEDLINE-96303695; PubMed-9723724;
Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E.,
Spanos S., Malley T., Gibbs R.A.;
A gene-ritch cluster between the CD4 and triosephosphate isomerase
genes at human chromosome 12p13.";
Genome Res. 6:314-326(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJNE-92141214; PubMed-1736296;
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"Isolation of a src homology 2-containing tyrosine phosphatase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Banville D., Stocco R., Shen S.H.; "Human protein tyrosine phosphatase 1C (PTPN6) gene structure:
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MEDLINE-98447672; PubMed-9774441;
                              Yi T., Cleveland J.L., Ihle J.N.;
"Protein tyrosine phosphatase containing SH2 of arracterization, preferential expression in localization to human chromosome 12p12-p13.",
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Nature 353:868-868(1991).
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MEDLINE-91343005; PubMed-1652101;
MEDLINE=92123209; PubMed=1732748;
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CMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSE-TRTI 351 TREVEKGRNKCVPYWPEVG-MQRAYGPYSVTNCGEHDTTEYKLRTLQVSPLDNGDLIREI YQFHYKNWPDHDVPSSIDPILELIWDVRCYQED - - DSVPICIHCSAGCGRTGVICAIVDY

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410 WHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVI---

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00383; TYR_HOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS50001: SH2; 2.
Hydrolase; SH2 domain; Repeat; Phosphorylation; Alternative splicing;
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SLSVR -> MLSRG (IN SHORT ISOFORM).
VR -> LSRG (IN REF. 2).
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PROTEIN-TYROSINE PHOSPHATASE.
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-> V (IN REF. 4).
-> E (IN REF. 5).
4D7736C21D3542D2 CRC64;
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InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000342; TYR_phosphatase.
InterPro; IPR000124; TYR_prot_phphtase.
Pfam; PF001017; SH2; 2.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
PRINTS; PR00401; SH2DOMAIN.
SMART; SM00194; PTPC; 1.
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SH2 2.
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U15533; AAA82879.1;
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1FPR; 07-MAR-01.
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Mol. Cell. Biol. 13:1497-1506(1993).
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1-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-
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244 TWMLLKDGIIPENFSVFSL-----IREMRTQRPSLVQTQEQYELVYNAV---LELF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro, IPR003961; FN_III.
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MGD; MGI:97814; Ptprg.
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75 LITSD-EDSSYINANFIKG-VYGP----KAYLATQGPLSTTLLDFWRMIWEYSVLIIVMA 128

15 QSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELS 74

13.4%; Score 485; DB 1; Length 595; 33.0%; Pred. No. 1.1e-22; tive 69; Mismatches 129; Indels

Conservative

Matches 128;

ò g ò

Query Match

Best Local

Similarity

us-09-600-358a-4.rsp

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                      PTPM_MOUSE
P28828;
                                                                                                RESULT 12
PTPM_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KECNKEKNRNSSVVPAERARVGLAPLPGMKGTDYINASYIMG-----YYRSNEFII 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEDEFVYWPSREES---MNCEAFTVTLISKDRLCLS------NEEQIIIHDFILEA 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:| : : | ||||||: | ||||||||| : || SRVKLRPLPGKDSKHSDYINANYVDGYNKAKAYIATQGPLKSTFEDFWRMIWEQNTGIII 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKV------ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 OMDVIRDKHSGTESOAKH-----CIPEKNHTLQADSYSPNLPKSTTKAAKMMNQQRTKM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIKESSSFDFRTSEI--SAKEELVLHPAKSSTSFDFLELNYSFDKNADTTMKWQTKAFPI 405
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                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 485; DB 1; Length 1442;
25.8%; Pred. No. 3.8e-22;
tive 96; Mismatches 263; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                KFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDY 68
                                                                                                                                                                                                                                           BY SIMILARITY.

ANCESTRAL ACTIVE SITE.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN-TYROSINE PHOSPHATASE GAMMA.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                         - 2
                                                                                                                                                                                                  CARBONIC-ANHYDRASE LIKE.
FIBRONECTIN TYPE-III.
PROTEIN-TYROSINE PHOSPHATASE
BY SIMILARITY.
                                       Pfami, FFOOUT, 100, 100 phatase; 2. Print, PFOOUT, 100 phatase; 2. PRINTS; PRO0700; PRTYPHPHTASE.
Prodom; PD000865; Carb_anhydrase; 1. SMART; SM00060; FN3; 1. SMART; SM00194; PTPC; 2. PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50055; TYR_PHOSPHATASE_1; 2. PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2. Glycoprotein; Transmembrane; Hydrolase; Repeat; Signal. SIGNAL
                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00194; carb_anhydrase; 1.
Pfam; PF00041; fn3; 1.
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1442 AA;
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Matches 160;
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DOMAIN
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ACT_SITE
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                                                         1300 TQDDYVLEVRHFQCPKWPNPDAPISSTFEL----INVIKEEALTRDGPTIVHDEYGAVSA 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 - protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.1.3.48) (R-PTP-MU)
526 VY-SYIPLVENPYFSSWPPSGTSSKMSLDLPEKQDGTVFPSSLLPTSSTSLFSYYNSHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: MOST ABUNDANT IN LUNG, LESS IN BRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 MAM DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Protein-tyrosine phosphatase MU precursor (EC
                                                                                                                                                                                                                                                                                                                                                1452 AA
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Interpro; IPR000387; TYR_phosphatase.
Interpro; IPR000242; Tyr_prot_phphtase.
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InterPro; IPR003962; FnIII_repeat.
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Pfam; PF00102; Y_phosphatase;
PRINTS; PR00104; FNTYPEIII.
PRINTS; PR00020; MAMDOMAIN.
PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                            | : | : | | | 1:1|
1356 GMLCALTTLSQQLENENAV 1374
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InterPro; IPR003006; Ig_MHC.
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                                                                                                                            585 LSLNSPTNISSLLNQESAV
                                                                                                                                                                                                                                                                                                                                                STANDARD;
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SMART; SM00409; IG; 1.
SMART; SM00137; MAM; 1.
SMART; SM00194; PTPC; 2.
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HSSP; P28827; 1RPM.
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Pfam; PF00047; iq; 1
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4;
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein-tyrosine phosphatase zeta precursor (EC 3.1.3.48) (R-PTP-zeta) (Phosphacan) (3FB chondroitin sulfate proteoglycan).
                                                                                                                                                                                                                                                                                                                                                                                               PYHATGLLGFVRQVKSKSPPNAGPLVVHCSAGAGRTGCFIVIDIMLDMAEREGVV----D 1122
                                                                                                                                                                                                                                                                                                                                                                 DSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVWACMEYEMGKKKCE 140
                                                                                                                                                                                                                                                                                                                                    RYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNS--ETRTIYQFHYKNWPDHDV 198
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                          KEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDE 80
                                                                                                                                                                                                                                                                                                                                                                                                                      PSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFS
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(POTENTIAL)
(POTENTIAL)
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                                                            PROTEIN-TYROSINE PHOSPHATASE MU. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                             DB 1; Length 1452;
                                                                                                                              FIBRONECTIN TYPE-III 4.
PROTEIN-TYROSINE PHOSPHATASE
PROTEIN-TYROSINE PHOSPHATASE
                                     Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                            98; Indels
                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                        FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
                                                                                                 IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                       F99D0FC67922CF1E
                                                                                                                                                                  POTENTIAL.

N-LINKED (GLCNAC.

N-LINKED (GLCNAC.
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Pred. No. 9e-22;
                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                            57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 VFSLIREMRTQRPSLVQTQEQYELVYNAVLE 289
       TYR_PHOSPHATASE_2; 2.
TYR_PHOSPHATASE_PTP;
                                                    POTENTIAL
                                                                                                                                                                                                                                                              N-LINKED
                                            Repeat
                                                                                                                                                                                                                                                                                            13.3%;
35.4%;
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                      PROSITE; PS00740; MAM_1; 1
PROSITE; PS50060; MAM_2; 1
                                                                                                                                                                                                                                                                                                            Conservative
                                             domain;
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1447
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1389
260
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534
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651 69
681 68
1452 AA;
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              PS50055;
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414
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MEDLINE-94216329; PubMed-7512960; Grumet M., Milev P., Sakurai T., Karthikeyan L., Bourdon M., Margolis R.U.; Margolis R.U.; "Interactions with tenascin and differential effects on cell adhesion of neurocan and phosphacan, two major chondroltin sulfate proteoglycans of nervous tissue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milev P., Friedlander D.R., Sakurai T., Karthikeyan L., Flad M., Margolis R.U.;
Margolis R.K., Grumet M., Margolis R.U.;
"Interactions of the chondroltin sulfate proteoglycan phosphacan, the extracellular domain of a receptor-type protein tyrosine phosphatase, with neurons, glia, and neural cell adhesion molecules.";
J. Cell Biol. 127:1703-1715(1994).
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SUBUNIT: THE CARBONIC-ANHYDRASE LIKE DOMAIN BINDS TO CONTACTIN.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: A LONG FORM (SHOWN HERE), A SHORT FORM
MISSING AN INTERNAL SEGMENT, AND PHOSPHACAN WHICH REPRESENTS THE
ENTIRE EXTRACELULAR DOMAIN ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: NERVOUS TISSUE-SPECIFIC.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC-
TYPE CARBONIC ANHYDRASE FAMILY.
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The carbonic anhydrase domain of receptor tyrosine phosphatase beta
is a functional ligand for the axonal cell recognition molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s:
                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence and molecular variants of rat receptor-type protein tyrosine phosphatase-zeta/beta.";
DNA Seq. 5:323-328(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=SPRAGUE-DAWLEY; TISSUE-Brain;
MEDLINE=94195772; PubWed=7511813;
Maurel P., Rauch U., Flad M., Margollis R.K., Margollis R.U.;
Phosphacan, a chondroitin sulfate proteoglycan of brain that interacts with neurons and neural cell-adhesion molecules, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95354206; PubMed=7628014;
Peles E., Nativ M., Campbell P.L., Sakurai T., Martinez R., Lo
Clary D.O., Schilling J., Barnea G., Plowman G.D., Grumet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             extracellular variant of a receptor-type protein tyrosine phosphatase.";
                                                                                                                                                                                                                                                                                                        Maurel P., Meyer-Puttlitz B., Flad M., Margolis R.U., Margolis R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (PHOSPHACAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 91:2512-2516(1994).
                                                                                                                                                                                                         SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
MEDLINE-96063026; PubMed-7579589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING TO N-CAM AND NG-CAM (PHOSPHACAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 269:12142-12146(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95096181; PubMed-7528221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING TO TENASCIN (PHOSPHACAN).
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PTPRZ OR PTPZ
                                        norvegicus (Rat)
                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlessinger J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphatase.
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CHONDROITIN SULFATE (POTENTIAL).
BY SIMILARITY.
ANCESTRAL ACTIVE SITE.
N-LINKED (GLCNAC...) (POTENTIAL).
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PROTEIN-TYROSINE PHOSPHATASE
PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN SHORT ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
Signal; Glycoprotein; Transmembrane; Hydrolase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBONIC-ANHYDRASE LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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MISSING (IN PHOSPHACAN
                                                                                                                                                                                           InterPro; IPR003961; FN_III.
InterPro; IPR000387; TR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00194; carb_anhydrase; 1.
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                                                                                                                                                                                                                                                       Pfam; PF00041; fn3; 1, Pfam; PF00102; Y_phosphatase; 2. PRINTS; PR00700; PRTYPHPHTASE. ProDom; PD000865; Carb_anhydrase; 1.
                                                                                                                                                                                interPro; IPR001148; Carb_anhydrase.
                                                                                                                                   EMBL; U09357; AAC52207.1; -. EMBL; U04998; AAC52383.1; -.
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SMART; SM00060; FN3; 1.
SMART; SM00194; PTPc; 2
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SEQUENCE
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1819 HNVEVIVMITHLVEKGRRKCDQYW--PTDGSEEYGSFLVNQKNVQVLAYYTVRNFTLRNT 1876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETA-CATENIN MAY BE A SUBSTRATE FOR THE CATALYTIC ACTIVITY OF PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine + phosphate.
SUBCELUIAR LOCATTON: Type I membrane protein.
TISSUE SPECIFICITY: HIGH LEVELS IN LIVER AND KIDNEY. LOWER LEVELS IN LUNG, BRAIN AND HEATH. NOT SEEN IN SPLEEN AND TESTIS.
DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED WITH HIGHEST
                                                                                                                                                                                                                                                                                                                                                                                                                                     290 LFKRQMDVIRDKH-----NLP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 KSTTKAAKMMNQQRTKMEIKESSSFD-----FRTSEISAKEELVLHPAKSSTSFD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LQKHQ 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang Y.P., Wang H., D'Eustachio P., Musacchio J.M., Schlessinger J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of R-PTP-kappa, a new member of the receptor protein tyrosine phosphatase family with a proteolytically cleaved cellular adhesion molecule-like extracellular region."; Mol. Cell. Biol. 13:2942-2951(1993).
-!- FUNCTION: REGULATION OF PROCESSES INVOLVING CELL CONTACT AND ADHESION SIGH AS GROWTH CONTROL, TUMOR INVASION, AND METASTASIS. PORMS COMPLEXES WITH BETA-CATENIN AND GAMMA-CATENIN/PLAKOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 - protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein-tyrosine phosphatase kappa precursor (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                          120 YSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPF----SVSCEAEKRKSDYIIRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                      230 GCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLE
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2 DQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYK
                                                                                   DILPYDYSRVELSLITSDED -- SSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWE
                                                                                                                                                                                                                                                                175 KVKFNSET-----RTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSA
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STRAIN-RI; TISSUE-Brain;
MEDLINE-93233655; Pubmed-8474452;
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01-JUN-1994 (Rel. 29, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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PTPRK OR PTPK.
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P35822;
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PTPK_MOUSE
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19;

90; Mismatches 182; Indels 114; Gaps

Matches 142; Conservative

Similarity

Query Match

Best Local

13.3%; Score 479; DB 1; Length 2316; 26.9%; Pred. No. 1.7e-21;

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SEQUENCE
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                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            DEVELOPMENTAL PLASTICITY.
PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
SIMILARITY: CONTAINS 1 MAMUNGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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 EXPRESSION FOUND IN DEVELOPING AREAS OR IN AREAS CAPABLE OF
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SIMILARITY.
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N-LINKED
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                                                                                                                                                                                                                                                             135 GKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIR--TLKVKFNSETRTIYQFHYKN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGGGRTGVICAIVDYTWMLLKDGI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 IPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLEL------FK-RQMDVIR 299
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                                                                                                                                                                                                                                                                                                                                                    81 DSSYINANFI-----KGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVWACMEYEM 134
                                                                                                                                                         93; Gaps
                                                                                                                                                                                                                         21 KEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDE 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain stem;

MEDLINE=92352948; PubMed=8387522;
Levy J.B., Canoll P.D., Silvennoinen O., Barnea G., Morse B.,
Honegger A.M., Huang J.-T., Cannizzaro L.A., Park S.-H., Druck T.,
Huebner K., Sap J., Ehrlich M., Musacchio J.M., Schlessinger J.;
"The cloning of a receptor-type protein tyrosine phosphatase "The cloning of a receptor-type protein tyrosine phosphatase J. Biol. Chem. 268:10573-10581(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 AAKMMNQQRTKM--EIKESSSFDFRTSEISAKEELVLHPAKSSTSFDFLELNYSF----
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-ULL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein-tyrosine phosphatase zeta precursor (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1289 VMLNEVDLSQGCPQYWPEEGMLRYGPIQVECMSCSMDCDVINRIFRICNLTRP 1341
                                                                                          Length 1457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DKNADTTMKWQTKAF----PIVGEPLQKHQSLDLGSLLFEGCSNSKP
                                                                                                                                                             Indels
1457 AA; 164185 MW; 19D4B99B7ECE8605 CRC64;
                                                                                          13.2%; Score 478.5; DB 1; 28.5%; Pred. No. 9.7e-22; tive 78; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 89:7417-7421(1992).
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MEDLINE=92366472; PubMed=1323835;
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                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate.
SUBUNIT: THE CARBONIC-ANHYDRASE LIKE DOMAIN BINDS TO CONTACTIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATUE PRODUCTS: 2 ISOPORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS SYSTEM, WHERE IT IS LOCALIZED IN THE PURKINE CELL LAYER OF THE CEREBELLUM, THE DENTATE GYRUS, AND THE SUBEPENDYMAL LAYER OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTERIOR HORN OF THE LATERAL VENTRICLE. DEVELOPMENTALLY REGULATED IN THE BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE FAMILY.
-1- SIMILARITY: CONTAINS 2 PROTEIN-TROSINE PHOSPHATASE DOMAINS.
-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-1- CAUTION: CALLED RPTPASE BETA IN REF. 2 AND 4.
                                                                                                                                                                                                                                                     Kaplan R., Morse B., Huebner K., Croce C., Howk R., Ravera M., Ratca G., Jaye M., Schlessinger J.;
"Cloning of three human tyrosine phosphatases reveals a multigene family of receptor-linked protein-tyrosine-phosphatases expressed in brain.";
                                                                                   Krueger N.X., Streuli M., Saito H.;
"Structural diversity and evolution of human receptor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE ZETA.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).
-!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF SPECIFIC
DEVELOPMENTAL PROCESSES IN THE CNS.
                                                                                                                                                                                        SEQUENCE OF 1749-1990 AND 2047-2280 FROM N.A. (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMOODOS, FURTHER, SMOOD STATES, 1.
SMART; SMOOD STATES, 1.
PROSITE; PSOOD STATE, PHOSPHATASE_1; 1.
PROSITE; PSSOOS; TYR_PHOSPHATASE_1; 2.
PROSITE; PSSOOS; TYR_PHOSPHATASE_PTP; 2.
SIGNAL; Glycoprotein; Transmembrane; Hydrolase; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                    OF 1479-2091 FROM N.A. (LONG FORM)
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InterPro: IPR003961; FN_III.
InterPro: IPR003867; TYR_phosphatase.
InterPro: IPR000342; TYR_prosphatase.
Pfam; PF00194; carb_anhydrase; 1.
Pfam; PF00102; Y_phosphatase; 2.
PRIMTS; PR00700; PRTYPHPHTASE.
ProDom; PD000865; Carb_anhydrase; 1.
                                                                                                                                                                                                                                 MEDLINE-90384936; PubMed-2169617;
                                        TISSUE=Liver;
MEDLINE=91006018; Pubmed=2170109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M93426; AAA60225.1; -.
EMBL; X54135; CAA38070.1; -.
PIR; S12054; S12054.
PIR; A46151, A46151.
HSSP; P18052; IYFO.
MIM; 176891; -.
                                                                                                                              tyrosine phosphatases.";
EMBO J. 9:3241-3252(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1718 EEFETLKEFYQEVQSCTVD-----LGITADSSNHPDNK-------HKNRYI 1756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 YSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPF----SVSCEAEKRKSDYIIRTL 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVKFNSET-----RTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 GCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLE
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; Mismatches 192; Indels 112;
                                                                                                                                                                                                             (POTENTIAL)
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                                                          CHONDROITIN SULFATE (POTENTIAL).
CHONDROITIN SULFATE (POTENTIAL).
CHONDROITIN SULFATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%; Score 478; DB 1; Length 2314;
                                                                                                           CHONDROITIN SULFATE (POTENTIAL)
CHONDROITIN SULFATE (POTENTIAL)
                              PROTEIN-TYROSINE PHOSPHATASE 1. PROTEIN-TYROSINE PHOSPHATASE 2.
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CARBONIC-ANHYDRASE LIKE.
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ANCESTRAL ACTIVE SITE.
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                                                                                                                                                                                                                                                                                          GLCNAC.
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AA;
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Db 2164 LIIQDFILEATQDDYVLEV--RHFQCPKWPNPDSPISKT----FELI 2204

Search completed: May 26, 2002, 12:26:53 Job time: 538 sec

(OTARU) XNAJB 3DA9 21HT

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2002, 12:16:55; Search time 95.55 Seconds (without alignments)
1252.878 Million cell updates/sec
1 US-09-600-358A-4
Sequence: 1 MDQRELLOKFLDEAQSKKIT......RPSKSVKLRSPKSGKNFSWL 692
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 56222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 56222
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Database : SPTREMBL_19:*

1: Sp_archea:*
2: Sp_bacteria:*
4: Sp_fungi:*
4: Sp_human:*
5: Sp_invertebrate:*
6: Sp_mnamal:*
7: Sp_mhc:*
10: Sp_plage:*
10: Sp_plage:*
11: Sp_rodent:*
12: Sp_virus:*
13: Sp_vertebrate:*
14: Sp_unclassified:*
15: Sp_archius:*
16: Sp_bacteriap:*
17: Sp_archius:*
16: Sp_bacteriap:*
17: Sp_archeap:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	O95064 homo sapien	095063 homo sapien	09v2r2 homo sapien	09p0u2 homo sapien	063745 rattus norv	P70602 rattus norv	0922e3 mus musculu	Q61152 mus musculu	099952 homo sapien	Q9h0y6 homo sapien	Q16614 homo sapien	Q61373 mus musculu	Q9pum2 xenopus lae	Q62884 rattus norv	Q15255 homo sapien	O61812 mus musculu
	ΩI	095064	095063	Q9Y2R2	Q9P0U2	Q637451	P70602	Q922E3	061152	099952	09н0т6	016614	061373	Q9PUM2	062884	015255	061812
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	Length	692	808	807	799	382	453	453	453	458	1114	1143	361	1195	1216	1337	1291
% Query	Match	6.66	98.7	97.2	82.2	28.8	20.7	20.3	20.3	19.6	14.3	14.3	14.2	14.1	14.1	14.1	14.0
	Score	3611	3569	3512.5	2971.5	1042	748	735.5	733.5	708	515.5	515.5	513	511	508	508	507
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Gaps

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99.9%; Score 3611; DB 4; Length 692; 99.9%; Pred. No. 5.9e-249; Live 0; Mismatches 1; Indels (

Query Match Best Local Similarity 99.94 Matches 691; Conservative g G

8375848DF8D3D853 CRC64;

91763 MW;

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KDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEY 120
                                            ETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGGGRTGVICAI 240
                                                                                                       VDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRD 300
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          SVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNS
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Catarrhini; Hominidae; Homo.
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"Human cDNA of LyPl Protein Tyrosine Phosphatase.";
"Human cDNA of LyPl Protein Tyrosine Phosphatase.";
submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF001845. AAD00904.1;
HSSP; Q06124; 2SHP.
InterPro; IPR000347; TYR_phosphatase.
InterPro; IPR000342; Tyr_prot_phphtase.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
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Last annotation update)
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PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_TP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                            KDILPYDY SRVELSLITSDEDSSY INANFIKGVY GPKAY IATQGPLSTILLDFWRMIWEY
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                                                                         LLFEGCSNSKPVNAAGRYFNSKVPITRTKSTPFELIQQRETKEVDSKENFSYLESQPHDS
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Catarrhini; Hominidae; Homo.
                                                          1 MDQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRY
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                               Indels
   Length
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC.2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN TYROSINE PHOSPHATASE HOMOLOG.
HOMO sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae,
Score 3569; DB 4;
Pred. No. 7.1e-246;
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                              0; Mismatches
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 98.78;
99.98;
                                 Conservative
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                Similarity
                               684;
   Query Match
Best Local 3
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Q9Y2R2
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SAVLATAPRIDDEIPPPLPVRTPESFIVVEEAGEFSPNVPKSLSSAVKVKIGTSLEWGGT
                                                                              TISSUE-ADRENAL GLAND;
                                (Human)
                                                                                                                                                                                                   799 AA;
                                                                       SEQUENCE FROM N.A.
                                                       NCBI_TaxID-9606
                                Homo sapiens
01-OCT-2000
01-DEC-2001
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SEQUENCE
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                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                         1 MDQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRY
                                                                                                                                                                                          SVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNS
                                                                                                                                                                                                                          ETRIIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRIGVICAI
                                                                                                                                                                                                                                                                                VDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRD
                                                                                                                                                                                                                                                                                                                KHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQQRTKMEIKESSSFDFRTS
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                                                                                                                                                                                                                                                                                                                                                                                                                      SAVLATAPRIDDEIPPPLPVRTPESFIVVEEAGEFSPNVPKSLSSAVKVKIGTSLEWGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 807
                                                                                                                                    Indels
databases
                                                                                            91708 MW; A5B4B4CAB795E812 CRC64;
                                                                                                                    4;
                                                                                                                    97.2%; Score 3512.5; DB 4 98.8%; Pred. No. 7.5e-242;
EMBL/GenBank/DDBJ
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                   INCEPTO: 1PR000387; TYR_phosphatase.
InterPro: 1PR000242; Tyr_prot_phphtase.
InterPro: 1PR000242; Tyr_prot_phphtase.
Pfan; PR00102; Y_phosphatase; 1.
PRNINTS; SR00194; PTPC; 1.
PROSITE; PS500383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
                                                                                                                                    0; Mismatches
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Q9P0U2;
01-OCT-2000 (TrEMBLrel. 15,
     EMBL; AF077031; AAD27764.1;
HSSP; Q06124; 2SHP.
                                                                                                                            Local Similarity 90.0
nes 677; Conservative
                                                                                            807 AA;
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                                                                                     Hydrolase.
SEQUENCE
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Best Local S
Matches 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPPSGTSSKMSLDLPEKQDGTVFPSSLLPTSSTSLFSYYNSHSSLSLNSPTNISSLLNQE
                                                                                           Euteleostomi;
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                                                                                                                                                                                                     Jiang
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                 Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jia
Han Z., Wang Y., Chen Z., Fu G.;
"A novel gene expressed in human adrenal gland.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFISO732: AAF67472.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       93F5385016F33D0C CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PROTEIN TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.2%; Score 2971.5; DB 4 Best Local Similarity 87.3%; Pred. No. 2.6e-203; Matches 598; Conservative 17; Mismatches 61;
                                                                                                                                                                                                                                                                                                        InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR00042; TYR_prot_phphtase.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00194; PTPC; 1.
PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE: PS50056; TYR_PHOSPHATASE_2: 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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MEDLINE=97067206; PubMed=8910608;
Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
"The novel protein-tyrosine phosphatase PTP20 is a positive regulator of PC12 cell neuronal differentiation.";
J. Biol. Chem. 271:29422-29426(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETRIIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 VDYTWALLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKROMD---- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 VLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKR-KSDYIIRTLKVKFNS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DILPYDYSRYELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYS 121
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QREILQKFLDEAQSKKITKEE-FANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 LYQNLKENRAPICKDSSSLRTSSA---LPATSRPLGGVLRSISVPGPPTLPMADIYA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------PNLPKSTTESQAKHCIPEKNHTLQADSYS-----PNLPKSTTKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.7%; Score 748; DB 11; Length 4 43.1%; Pred. No. 3.18-45; ive 58; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Action (1) (2) SEQUENCE FROM N.A. Acki, N. Yamaguchi-Acki, Y. Ullrich A.; Submitted (2PP-1996) to the EMBL/GenBank/DDBJ databases. EMBL, U69673; AAC52896.1; HSSP; Q06124; ZSHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6CCC132206FB69AE CRC64;
                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000287; TYR_phosphatase.
InterPro; IPR000242; TYr_prot_phphase.
Pfam. PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00194; PTPC; 1.
PR051TE; PS500383; TYR_PHOSPHATASE_1; 1.
PR051TE; PS50055; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
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                                                                                                                                Created)
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                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last PROTEIN TYROSINE PHOSPHATASE 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 AA; 50106 MW;
                                                                                                                                (TrEMBLrel. 02,
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Best Local Similarity 43.18
Matches 154; Conservative
 -----DAKEEILQPP 356
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                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                             PRELIMINARY;
                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                              01-FEB-1997
                                                                                                                                                 01-FEB-1997
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                                                                                         P70602
P70602;
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ID Q9
AC Q9
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MEDLINE-95046282; PubMed-7957881;
MCDLINE-95046282: PubMed-7957881;
MCDLINE-95046282: Tubmed-7957881;
Takenaka T., Kamada N.;
"CDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kindney.";
FEBS Lett. 353:305-308(1994).
ESBS: DAMO7265.1; -.
HSSP; Q06124; 2SHP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 IWEYNVVIIVWACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQARTDYFIRTLLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 KFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGGGRTGV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDQREILQKFLDEAQSKKIT----KEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 382;
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                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.8%; Score 1042; DB 11;
ilarity 53.5%; Pred. No. 2.8e-66;
Conservative 62; Mismatches 89;
                                                                                                                                                                                       382 AA
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InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_prot_phphtase.
PRIMTS; PR00100; Y_phosphatase; 1.
PR011TE; PR000194; PTPC; 1.
PR05ITE; PS000383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
                                                                          SEPKKFDDSVILRPSKSVKLRSPKS 676
                                                       661 SEPKKFDDSVILRPSKSVKLRSPKS 685
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                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 201;
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303 SGTESQAKHCIP--EKNHTLQADSYSP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 144; Conservative
                                                                                                                                                   HEMATOPOIETIC CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
VARSPLIC
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                          124 IIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKR-KSDYIIRTLKVKFNSET 182
                                                                                                                                                                                                                                                                                                                                                                                        RTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVD 242
                                                                                                                                                                                                                                                                                                                                                                                                   YTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 YVROLLLTQTIPPNFSLEQVVLEMRKQRPAAVQTEGOYRFLYHTVAQLFSR---TLODTS 300
                                                                                                                                                                                                                                                                                                                                                        64 LPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVL 123
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                5 EILQKFLDEAQSKKITKEE-FANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDI 63
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                               6
                                                                                                                                                                                                         453;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE
                                                                                                                                                                                                         Length
                                                                                                                                                                                                                              65; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheng J., Daimaru L., Fennie C., Lasky L.A.;
"A novel protein tyrosine phosphatase expressed in
lin(lo)CD34(h1)Sca(h1) hematopoietic progenitor cells.";
                                                                                                                         Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC008512; AAH08512.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN-TYROSINE HOSPHARASE 18 (EC 3.1.3.48) (PTP-K1)
(FETAL LIVER PHOSPHARASE 1) (FLP1) (PTP 49) (PTP HSCF)
                                                                                                                                                                       453 AA; 50227 MW; 722FDE1FFC9F4689 CRC64;
                                                                                                                                                                                                        20.3%; Score 735.5; DB 11; 44.0%; Pred. No. 2.4e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 SGTESQAKHCIP--EKNHTLQADSYSP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 PHYQNLKENCAPICKEAFSLRTSSALP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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MEDLINE-96329547; Pubmed-8695832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97030045; PubMed=8875997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          061152 PRELIMINARY; P
061152; 062404;
01.NOV-1998 (TERBELFEL: 08, Cre
01-NOV-1998 (TERBELFEL: 08, Las
01-DEC-2001 (TERBELFEL: 19, Las
PROTEIN-TYROSINE PHOSPHATASE 18
                                                                                                                                                                                                                               Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blood 88:1156-1167(1996).
                                                         musculus (Mouse).
                                                                                                                                                                                                                   Local Similarity
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR PTPK1
                                                                                                                                                           Receptor
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                       183
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TYROSINE + PHOSPHATE.

C. -! - SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.

-! - SUBCELLULAR LOCATION: THO FORMS OF THE PROTEIN, FIPL AND FLP1B, MAX BE PRODUCED STATES ENPRESSED OF FIPE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF FIPLA.

-! - TISSUE SPECIFICITY: HIGHEST EXPRESSED IN BONE MARROW. ALSO EXPRESSED IN KIDNEY, LUNG, OVARY, SPLEEN, THYMUS AND LYMPH NODE.

-! - DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 15.5.

-! - SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-

TYROSINE PHOSPHATASE FAMILY.

REMBL: U35124; AAB18623.1; -.

REMBL: U35223; AAC52991.1; -.
                                                                                                                                                                                                                                            STRAIN-C57BL/6; TISSUE-FETAL LIVER;
MEDLINE-97131769; PubMed-8977243;
Dosil M., Leibman N., Lemischka I.R.;
"Cloning and characterization of fetal liver phosphatase 1, a nuclear protein tyrosine phosphatase isolated from hematopoletic stem cells.", Blood 88:4510-4525(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 VILMACQETENGRRKCERYWAREQE-PLKAGPFCITLTKETTLNADITLRTLQVTFQKEF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 EILQKFLDEAQSKKITKEE-FANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDI 63
                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::: ||:: ::: : | || :| :| :| :| |
6 DLVRSFLEQLEARDYREGAILAREFSDIKARSVAWKSEGVCSTKAGSRLGNINKNRYKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 YTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 RTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGGGRTGVICAIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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MGD; MGI:108410; Ptpn18.

InterPro; IPR000342; TYR_phosphatase.

R Pfam; PF0010.2; Z_phospbatase.

R Pfam; PF0010.2; Y_phosphatase.

R Pfam; PF0010.9; PRTPHPHTASE.

R PROSTTE; PS00343; TYR_PHOSPHATASE.1; 1.

R PROSTTE; PS50056; TYR_PHOSPHATASE.2; 1.

R PROSTTE; PS50056; TYR_PHOSPHATASE.2; 1.

R PROSTTE; PS50056; TYR_PHOSPHATASE.2; 1.

R PAGILISE; Nuclear protein; Alternative splicing.

Hydrolase; Nuclear protein; Alternative splicing.

PROPEINTYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.3%; Score 733.5; DB 11; Length 453; 44.0%; Pred. No. 3.4e-44;
cloning and characterization of PTP-K1, a novel nonreceptor tyrosine phosphatase highly expressed in bone marrow."; [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: MAY BE INVOLVED IN GROWTH AND DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGP -> LRRHRA (IN REF. 3)
88AD7E73CE8136B0 CRC64;
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MISSING (IN FLP1B).
F -> L (IN REF. 3).
ASAGTGP -> LRRHRA (3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO/SER/THR-RICH.
                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
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DQREILQK-------FLDEAQSKKITKEE--FANEFLKLKRQSTKYKADKTY 44
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Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
"Structural variants of human T200 glycoprotein (leukocyte-common
                             Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-PLACENTA;

MEDINE-99009912; Pubmed=2971730;

MEDINE., Streuli M., Schlossman S.F., Satto H.;

"Complete exon-introm organization of the human leukocyte common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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SMART; SM00194; PTPC; 2.
SMART; SM00404; PTPC_mCl; 2.
FNSOITE; PS00083; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003595; PTPc_motif.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen (CD45) gene.";
J. Immunol. 141:2781-2787 (1988).
EMBL, M23465, AAD15273.2;
EMBL, M23466, AAD15273.2;
EMBL, M23466, AAD15273.2;
EMBL, M23467, AAD15273.2;
EMBL, M23471, AAD15273.2;
EMBL, M23471, AAD15273.2;
EMBL, M23471, AAD15273.2;
EMBL, M23473, AAD15273.2;
EMBL, M23474, AAD15273.2;
EMBL, M23474, AAD15273.2;
EMBL, M23478, AAD15273.2;
EMBL, M23489, AAD15273.2;
EMBL, M23481, AAD15273.2;
EMBL, M23486;
EMBL, M23488;
EMBL,
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                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00700; PRTYPHPHTASE
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                                                                                                                                                                                                                                                                                                                  antigen).";
EMBO J. 6:1251-1257(1987).
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                       TISSUE-PLACENTA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim Y.W., Wang H.Y., Sures I., Lammers R., Martell K.J., Ullrich A.;
"Characterization of the PEST family protein tyrosine phosphatase
BDP1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 ANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.6%; Score 708; DB 4; Length 458; Best Local Similarity 46.7%; Pred. No. 2.2e-42; Matches 136; Conservative 54; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 AA; 50384 MW; 46BCA1E17C2C78B1 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T200 LEUKOCYTE COMMON ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN-TYROSINE-PHOSPHATASE (EC 31.3.48).
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PHYQNLKENCAPICKEAFSLRTSSALP 327
                                                                                                                                                                                       PRT;
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                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
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SEQUENCE
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Q9H0Y6
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DB4B4400F3602B3C CRC64;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                            PTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE=87275816; PubMed=2956090;
MEDLINE=87275816; PubMed=2956090;
Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
"Structural variants of human T200 glycoprotein (leukocyte-common "Structural")
                    SFIMSYWKPEVMIAAQGPL-KETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQ---YW
                                                 PLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEK
                                                            RKSDYIIRTLKV---KFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSV
                                                                                                       KMMNQQRTKMEIKESSSFDFRTSEISAKEELVL----HPAKSSTSFDFLELNYSFDKNA
                                                                                                                                                                                                                                             769 HIGNOEENKSKNRNSNVIPYDYNRVPLKHELEMSKESEHDSDESSDDDSDSEEPSKYINA
                                                                                                                                                                                                                                                                   393 DTTMK-WQTKAFPIVGEPLQKHQSLDLGSLLF-------EGCSNSKPVN
                                                                                                                                                                                                                                                                                                             434 AAGR--YFNSKVPITRT-KSTPFEL--IQQRETKEVDSKENFSY-----LESQPHD
                                                                                                                                     PICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPEN-FSVFSLIREMRTQRPSLVQTQEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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T200 LEUKOCYTE COMMON ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                        480 -SCFVEMQAQKVMHVSSAELNYSLPYDSKHQIRNASNVKHHDSSALGVY 527
                                                                                                                                                                                                                                                                                                                                                                             945 LISMIQVVKQKLPQKNSSEGN-------KHHKSTPLLIH 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
7200 LEUKCYTE COMMON ANTIGEN PRECURSOR.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; ITR003861; FN_III.
InterPro; ITR003861; FN_III.
InterPro; ITR003861; TYR_phosphatase.
InterPro; ITR000242; TYR_phosphatase.
Pfam: PF001041; fn3: 2.
PRINTS; PR00102: Y_phosphatase; 2.
PRINTS; PR00106: PRTYPHPHTASE.
SMART; SM00104; PTPC; 2.
PROSITE: PS000383: TYR_PHOSPHATASE_1; 2.
PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.
PROSITE: PS00056; TYR_PHOSPHATASE_PTP; 2.
Hydrolase; Signal.
Signal.
CHAIN
24 1143 T200 LEUKOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1143 AA
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EMBO J. 6:1251-1257(1987).
EMBL; Y00062; CAA68269.1; -.
HSSP; P18052; 1YFO.
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Higashitsuji H., Arii S., Furutani M., Imamura M., Kaneko Y.,
Takenawa J., Nakayama H., Fujita J.;
"Enhanced expression of multiple protein tyrosine phosphatases in the regenerating mouse liver : Isolation of PTP-RL 10, a novel
cytoplasmic-type phosphatase with sequence homology to cytoskeletal protein 4.1."
                                                                                                                                              504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             858 SFIMSYWKPEVMIAAQGPL-KETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQ---YW 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                 44
                                                                                                 DQREILQK-------FLDEAQSKKITKEE--FANEFLKLKRQSTKYKADKTY
                                                                                                                                            451 EQQELVERDDEKQLMNVEPIHADILLETYKRKIADEGRLFLAEFQSIPRVFSK----F
                                                                                                                                                                                              PITVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQG
                                                                                                                                                                                                                    RCPDYIIQKLNIVNKKEKATGREVTHIQFTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPEN-FSVFSLIREMRTQRPSLVQTQEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 KMMNQQRTKMEIKESSSFDFRTSEISAKEELVL----HPAKSSTSFDFLELNYSFDKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 AAGR--YFNSKVPITRT-KSTPFEL--IQQRETKEVDSKENFSY------LESQPHD
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                          PLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEK
                                                                                                                                                                                                                                                                                                                                                                                         RKSDYIIRTLKV---KFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSV
                                                  97;
     Length 1143;
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                                                  Indels
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Last annotation update)
                                               87; Mismatches 238;
  Score 515.5; DB 4 Pred. No. 3.9e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
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EMBL, D49393; BAA08386.1; -.
HSSP; P18052; 1YFO.
Query Match
Best Local Similarity 28.4%;
Matches 167; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                              YDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLII 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 VMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSETR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 TIYQFHYKNWPDHDVPSSIDPILELIWDVRCY--QEDDSVPICIHCSAGCGRTGVICAIV 241
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                      15 QSKKITKEEFANEFLKLKRQST----KYKADK----TYPTTVAENAKNIKKNRYKDILP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia; Batrachia, Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 RLIYQIENENTV----DVYGIVYDLRMHRPLMVQTEDQYVFLNQCVLDIIRAQKD 328
                                                                                                                                                                                                                                                                                                                 20;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RECEPTOR PROTEIN TYROSINE PHOSPHATASE RHO PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 361;
                                                                                                                                                                                                                                                                                                               50; Mismatches 110; Indels
                                                                                                                                                                           Hydrolase. _ _ non_rer 1 1 SEQUENCE 361 AA; 41726 MW; B51462E8D11023AA CRC64;
                                                                                                                                                                                                                                                                           14.2%; Score 513; DB 11; 39.0%; Pred. No. 1.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1195 AA
MGD; MGI:104574; Ptprj.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR000242; Tyr_proc_phphtase.
Pfam; PF00102; Y_phosphatase. 1.
PRINTS; PR00109; PRIYPHPHTASE.
SMART; SM00194; PTPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Achopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                               Best Local Sim
Matches 115;
                                                                                                                                                                                                                                                                           Query Match
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| || : ::||||| | : :||||| || 1025 GDIKVSAIETERPASYIIRTFTVQKKGSHEIREIRQFHFTSWPDNGVPCYATGLLGFIRQ 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 YGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR PROTEIN TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 VRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRP
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DENSITY-ENHANCED PHOSPHATASE-1 PRECURSOR (EC 3.1.3.48) (DEP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.1%; Score 511; DB 13; Length 1195; 41.5%; Pred. No. 8.7e-28; tive 47; Mismatches 92; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1195 1195
1195 AA; 132818 MW; 71F3C6D0AAD34F07 CRC64;
Pfam; PF00041; fn3; 3.
Pfam; PF00629; MAM; 1.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00100; MAMDOMAIN.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00100; PRTYPHPHTASE.
SMART; SM00137; MAM; 1.
SMART; SM00194; PTPC; 1.
PROSITE; PS00740; MAM_1; UNKNOWN_1.
PROSITE; PS00740; MAM_2; 1.
PROSITE; PS00066; MAM_2; 1.
PROSITE; PS00086; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
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1141 NMVQTEEQYVFVHDAILE 1158
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21 >1195
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                                                                     Interpro; IPR0003967; TR_LII.

R Interpro; IPR000342; TYR_phosphatase.

R Interpro; IPR000342; TYR_phosphatase.

R Interpro; IPR000342; TYR_phosphatase.

R Interpro; IPR000342; TYR_phosphatase.

R Ffam; PF00102; Y_phosphatase; 1.

R SMART; SM00106; FRIYPHPHTASE.

R SMART; SM00194; PTPC; 1.

R PROSITE; PS50056; TYR_PHOSPHATASE_1; FALSE_NEG.

R PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.

R PROSITE; PS50055; TYR_PHOSPHATASE_2? 1.

R PROSITE; PS50055; TYR_PHOSPHATASE_2PTP; 1.

R PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.

R SIGNAL

SIGNAL

SIGNAL

T SIGNAL

T SIGNAL
      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: HIGH EXPRESSION IN THE CEREBELLUM, BRAIN
CORTEX, AND KIDNEY CORTEX, AND SOMEWHAT LESS ABUNDANT IN SPLEEN
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                                      -!- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
EMBL; U40790; AAB53195.1; -.
HSSP; P18052; IYFO.
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN TYPE-III.
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                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
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TYROSINE + PHOSPHATE
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162
184
256
251
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663 66
669 66
703 70
789 78
816 81
                                 AND LUNG.
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a novel protein-tyrosine phosphatase, HPTPeta.";
Blood 84:4186-4194(1994).
EMBL; D37781; BAA07035.1; -.
                                                                                                                                                                                                                                    126 VMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSETR 183
                                                                                                                                                                                                                                                                                                            184 TIYQFHYKNWPDHDVPSSIDPILELIWDVRCY--QEDDSVPICIHCSAGCGRTGVICAIV 241
                                                                                                                  896 KSKLIRVENFEAYFKKQQADSNCGFAEEYEDLKLIGISLPKYAAEIAENRGKNRYNNVLP 955
                                                                                                                                                        66 YDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLII 125
                                        Gaps
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                                                                              15 QSKKITKEEFANEFLKLKRQST----KYKADK----TYPTTVAENAKNIKKNRYKDILP 65
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                                                                                                                                                                                                                                                                                                                                                                                                           : : : : | | : : | | | 1114::| | : | | | 1183 RLIYQIENENTV----DVYGIVYDLRMHRPLAWQTEDQYVFLNQCVLDIIRAQKD 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         242 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                        20;
Length 1216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.1%; Score 508; DB 4; Length 1337; 38.3%; Pred. No. 1.7e-27; Live 51; Mismatches 111; Indels 2
                                        Indels
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Last annotation update)
                                      51; Mismatches 110;
  14.1%; Score 508; DB 11; 38.6%; Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN-TYROSINE PHOSPHATASE PRECURSOR.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-95086212; PubMed-7994032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 38.3% Matches 113; Conservative
                                    Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                      Best Local Similarity
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Q15255;
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Search completed: May 26, 2002, 12:26:01 Job time: 546 sec

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1 601790135F1 NCI_CGA
3 daa36e12.yl NICHD X
5 da83f69.yl Harland
4L555127 LTI_NFL006
1 un16c07.yl Sugano m
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/PRELIQORETKEVDSKENFSYLESQPHBSCFVEWQAQKVWHYSSAELNYSLPPSSIL
                                                                                                                                                                                              AF077031 2903 bp mRNA linear HTC 22-MAY-2001
Homo sapiens protein tyrosine phosphatase homolog mRNA, complete
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FIVVEEAGEFSPNVPKSLSSAVKVKIGTSLEWGGTSEPKKFDDSVILRPSKSVKLRSP
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TSGKSFTRSKSLKILRNMKKSICNSCPPNKPAESVQSNNSSSFLNFGFANRFSKPKGP
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 2903)

Liu,T., Zhang,J., Fu,G., Zhang,Q., Ye,M., Zhou,J., Wu,J., Shen,Y., Yu,M., Chen,S., Mao,M. and Chen,Z.

Human protein tyrosine phosphatase (70zpep) homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-JUL-1998) Shanghai Institute of Hematology, Shanghai
Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P.R. China
Location/Qualifiers
    BF144494 (BG234079 CAW766206 CAM555127 AM319424 U
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Liu,T.
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3 AW676100 UT-HF BND-all-h-10 O-U
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| B1686558 603313654F1 NCI_CGAP_N
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a AF077031 Homo sapiens protein i BA48847 AGENCONFT_6413950 NIH i BG541535 602570982Fl NIF_MGC_77 AU132052 NUT2RP3 Homo s
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Database: EST:*
Database sequences: 13736207
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Page 2

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367	uLeuValLeuHisProalaLysSerSerThrSerPheAspPheLeuGluL 384	
384	euasnTyrSerPheaspLysasnalaaspThrThrMetLysTrpGlnThr 400 	
401	LysalapheprollevalGlyGluProLeuGlnLysHisGlnSerLeuAs 417	
417	PLEUGlySerLeuLeuPheGluGlyCysSerAsnSerLysProValAsnA 434 	
434	laalagiyargtyrPheasnSerLysValProIleThrargThrLysSer 450 	
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484	lumetGlnalaGlnLysValmetHisValSerSeralaGluLeuasnTyr 500 	0
501	SerLeuproTyrAspSerLysHisGlnIleArgAsnAlaSerAsnValLy 517 	7
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AGENCOURT_6413950 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5497108
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1 (bases 1 to 1116)

Nith-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality Sequence stop: 717.

Location/Qualifiers

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//tissue tvoe="INAGE:5497108"

//tissue tvoe="INAGE:5497108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lymphoma, cell line"
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/lab_host="DH10B (phage-resistant)"
/note="Gorgan: lymph; Vector: pCMV-SpoRT6; Site_1: NotI;
Site_2: Sall; cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
// Site_2: 232 g 302 t
                                                                                                                                   1920 ACTICCTGTATGGACACCTGAATCATTTATTGTGGTTGAGGAAGCTGGAG 1969
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Percent Identity: 78.960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5', mRNA sequence.
BM458477
BM458477.1 GI:18507517
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Quality: 1578.00
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US-09-600-358A-4 x BM458477
                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est2:BM458477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS BM458477
DEFINITION AGENCOURT_641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
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KEYWORDS
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ORIGIN
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AUTHORS
TITLE
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5 ATGGACCAAAGAAAATTCTGCAGAAGTTCCTGGATGAGGCCCAAAGCAA 1:	24
17 sLysIleThrIysGluGluPheAlaAsnGluPheLeuLysLeuLysArgG 34	74
34 InserThrLysTyrLysAlaAspLysThrTyrProThrThrValAlaGlu 50 	0 24
51 ASDALALYSASDILLELYSKSSBARGTYTLYSASPILELEUPTOTYFAS 67 :::	74
67 pTyrSerArgValGluLeuSerLeuIleThrSerAspGluAspSerSerT 84	24
<pre>lTyrGlyProLysAlaTyrIle 1 </pre>	00
lyProLeuSerThrThrLe 	17
laCysMetGluTyrGluM 1 	34
134 etGlyLysLysLysCysGluArgTyrTrpAlaGluProGlyGluMetGln 15 	50
151 LeuGluPheGlyProPheSerValSerCysGluAlaGluLysArgLysSe 16	67
167 raspTyrIleIleArgThrLeuLysValLysPheAsnSerGluThrArgT 18 	84 24
184 hrIleTyrGlnPheHisTyrLysAsnTrpProAspHisAspValProSer 20 	00
201 SerIleaspProIleLeuGluLeuIleTrpaspValargCysTyrGlnGl 21	17
217 uAspAspSerValProlleCysileHisCysSerAlaGlyCysGlyArgT 23 	34
leValAspTyrThrTrpMetLeuLeuLysAsp 2. 	50
1yIleIleProGluAsnPheSerValPheSerLeulleArgGluMetAr 2	67
8 8	
7 gThrGlnArgProSerLeuValGlnThrGlnGluGlnTyrGluLeuValT 2	
24	24
284 YIASHATAVALLEUGIULEUFNELYSALGGILMECKASPVALLIERIGASP 30 824	2 5
1 LysHisSerGlyThrGluSerGlnAlaLysHisCysIleProGluLysAs 3	17

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196
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                                                                                Ratio: 5.032
Percent Similarity: 99.103
                                                                 Quality: 1112.00
                                                                                                                                               US-09-600-358A-4 x BG541535
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LOCUS AU132052
                                                  alignment_scores
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   ORIGIN
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LOCUS BG341535
DEFINITION 602570982F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695140 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. L (bases 1 to 832)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nlh.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM1520 row: d column: 21
High quality sequence stop: 785.
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                                                                                                                                                                                                                                            367 luLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuGlu 383
                                                                                                                                                                                                                                                                                                            384 LeuAsnTyrSerPheAspLysAsnAlaAspThrThrMetLysTrpGlnTh 400
906 CAAAGCCGCAAAAATTGATGAACCACCAAAGGACAAAAAATGAATCAAA
                                                                                                                                                                               351 GluSerSerSer.PheAspPheArgThrSerGluIleSerAlaLysGluG
                                                                                                              334 hrLysAlaAlaLysMetMetAsnGlnGlnArgThrLysMetGluIleLys
                                                317 nHisThrLeuGlnAlaAspSerTyrSerProAsnLeuProLysSerThrT
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BG541535.1 GI:13533768
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EST 24-OCT-2000 580 400 613 630 500 900 LysLysPheAspAspSerVallleLeuArgProSerLys.SerValLysL 680 150 563 300 597 uGluAlaGlyGluPheSerProAsnValProLysSerLeuSerSerAlaV 647 497 51 TIGITITGIAGAGATGCAGGCTCAAAAAGTAATGCATGTTTCTTCAGCAG 100 linear nSerHisSerSerLeuSerLeuAsnSerProThrAsnIleSerSerLeuL ||||||||| |TCACATGATTCTTTATCACTGAATTCTCCAACCAATATTTCCTCACTAT 451 ATCCCCCTCCACTTCCTGTACGGACACCTGAATCATTTATNGTGGTTGA 647 alLysValLysIleGlyThrSerLeuGluTrpGlyGlyThrSerGluPro rCysPheValGluMetGlnAlaGlnLysValMetHisValSerSerAlaG luLeuAsnTyrSerLeuProTyrAspSerLysHisGlnIleArgAsnAla SerAsnValLysHisHisAspSerSerAlaLeuGlyValTyrSerTyrIl eProLeuValGluAsnProTyrPheSerSerTrpProProSerGlyThrS euAsnGlnGluSerAlaValLeuAlaThrAlaProArgIleAspAspGlu IleProProTeuProValArgThrProGluSerPheIleValValGl 551 TGAAGGTAAAATTGGAACATCACTGGAATGGGGTGGAACATCTGAACCA Percent Identity: 98.206 mRNA Gaps: ďq to:

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133 GluMetGlyLysLysLysCysGluArgTyrTrpAlaGluProGlyGluMe 149
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                                                                                                                                                                                                                                                                                                                     199
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                                                                                                                                                                                                                                HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Contact: Laboratory
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3952
Email: genomics@hri.co.jp
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Madical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="Nt72Rp3003698"
/coll_type="teratocarcinoma"
/cell_type="Nt2"
/note="Vector: pWE18SFL3; mRNA from NT2 neuronal precursor cells after 2 veeks retinoic acid (RA) induction"
= 132 c 162 9 217 t 4 others
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ tbase] to 796] Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
AU132052 NT2RP3 Homo sapiens cDNA clone NT2RP3003698 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 yrAspTyrSerArgValGluLeuSerLeuIleThrSerAspGluAspSer 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 ArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThrThrValAl 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 aGluAsnAlaLysAsnIleLysLysAsnArgTyrLysAspIleLeuProT 66
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Percent Identity: 66.535
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                                    AU132052
AU132052.1 GI:10992406
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4.187
87.402
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US-09-600-358A-4 x AU132052
                                                                                                          Homo sapiens
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HRI human
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                                                                                        human.
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BM469079 1003 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6445886 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:5587352
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1003)
NHT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Oppublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arroc
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LiAM12356 row: 1 column: 09
High quality sequence stop: 728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgThrIleTyrGlnPheHisTyrLysAsnTrpProAspHisAspValPr
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|||||||||:::||| ||||||||:::::|||| |||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 sAspGlyIleIleProGluAsnPheSerValPheSerLeuIleArgGluM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 etArgThrGlnArgProSerLeuValGlnThrGlnGluGlnTyrGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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BM469079
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DEFINITION
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AUTHORS
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
### This is a NIH_MC Library."
### 196 c 203 g 269 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 GluLysArgLysSerAspTyrIleIleArgThrLeuLysValLysPheAs 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 nSerGluThrArgThrIleTyrGlnPheHisTyrLysAsnTrpProAspH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 AAATGAATCTCGTAGGCTGTATCAGTTTCATTATGTGAACTGGCCAGACC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 IleArgGluMetArgThrGlnArgProSerLeuValGlnThrGlnGluG1 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 roGlyGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAla 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #||::: :::::||||||:: 305 GAACAAGAAGAAGAATTCATCATCAGGACACTCTTACTTGAATTTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 isAspValProSerSerIleAspProIleLeuGluLeuIleTrpAspVal 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 ATTTACTAAAAGCTGGGAAAATACCAGAGGAATTTAATGTATTTAATTTA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 CAAAAGCATATGTAGCAACTCAAGGACCTTTAGCAAATACAGTAATAGAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 IleLeuProTyrAspTyrSerArgValGluLeuSerLeulleThrSerAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roLysAlaTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAsp
||||||||||||::::||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 ArgCysTyrGlnGluAspAspSerValProIleCysIleHisCysSerAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 AGGAAATATCAAGAACATGAAGATGTTCCTATTTGTATTCATTGCAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 CTACTGCCATTTGATCACAGCCGAGTTAAATTGACATTAAAGACTCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 PheTrpArgMetileTrpGluTyrSerValLeuIleIleValMetAlaCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 etLeuLeuLysAspGlyIleIleProGluAsnPheSerValPheSerLeu
                                                                                                                                                                                                                                                                                          Length: 279
Gaps: 4
Percent Identity: 60.215
                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1003
/clone="IMAGE:5587352"
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                                                                                                                                                                                                                                                                                                             3.857
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                                                                                                                                                                                                                                                                                        887.00
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                                                                                                                                                                                       BASE COUNT
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582 bp mRNA linear EST 01-JUN-2000 EST379675 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence. AW967600. GI:8157437
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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assessment of gene expression patterns in a model of col-
metastsus using a 19,200 element cDNA microarray
Unpublished (2000)
Contect: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502 LeuProTyrAspSerLysHisGlnIleArgAsnAlaSerAsnValLysHi 518
                                             279 nTyrGluLeuValTyrAsnAlaValLeuGluLeuPheLysArgGlnMetA 296
296 spVal.....LysHis
                                                                                                                                                                         303 SerGlyThrGluSerGlnAlaLySHisCysIleProGluLysAsnHisTh
                                                                                                                                                                                                                                                               752 ATTAACACTGAAAACATGGTCAGCTCCATAGAGCCTGAAAAACAA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652 ATATGAACTTGTTCATAGAGCTATTGCCCAACTGTTTGAAAAACAGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 94.505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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137 c 101 g 180 t
                                                                                                                                                                                                                                                                                                                                              797 .....GATTCTCCCTCCTCAAANCACCNAGG 823
                                                                                                                                                                                                                                                                                                          319 rLeuGlnAlaAspSerTyrSerProAsnLeuProLys 331
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1. .582
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4.879
97.802
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                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AW967600
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AU132040 HIZRP3 Homo sapiens CDNA clone NT2RP3003678 5', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/lab_host="DH10B (LTI)"
//note="Vector: py773-Pez; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
8 87 c 115 g 139 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 LysAlaTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAspPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 etGluTyrGluMetGlyLysLysCysGluArgTyrTrpAlaGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 TGGAGTATGAAATGGGAAAGAAAAGAAAGTGTGTGAGCGCTACTGGGCTGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 GGAGAGATGCAGCTGGAATTTGGCCCTTTCTCTGTATCCTGTGAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 uLysArgLysSerAspTyrIlelleArgThrLeuLysValLysPheAsnS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erGluThrArgThrIleTyrGlnPheHisTyrLysAsnTrpProAspHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 AspValProSerSerIleAspProIleLeuGluLeuIleTrpAspValAr
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                                                                                                                                                                                                                                                                                                                                                                          10 AAGGCTTATATTGCCACCCAGGGTCCTTTATCTACAACCCTCCTGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 GlyGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 156
Gaps: 1
Percent Identity: 99.359
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                                                                                                                                                                                              848.50
5.474
99.359
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US-09-600-358A-4 x AW504119
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                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                Ratio:
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                                                                                                          BASE COUNT
ORIGIN
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KEYWORDS
SOURCE
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        End it cgapbs remain. In the year in the sequence.

End it site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/Dbrp/image/image.html

Location/Qualifiers
                                                                                                                                                                                                                               100 ATCCTTATTTTCATCATCATGGCCTCCAAGTGGTACCAGTTCTAAGATGTCT 149
                                                                                       585
                                                                                                                                                               601
                                                                                                                                                                                                                                                                                                                                                      heSerProAsnValProLysSerLeuSerSerAlaValLysValLysIle 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 TCTCACCAAATGTTCCCAAATCCTTATCCTCAGCTGAAGGTAAAATT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyThrSerLeuGluTrpGlyGlyThrSerGluProLysLysPheAspAs 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uProThrSerSerThrSerLeuPheSerTyrTyrAsnSerHisSerL
                                                                       LeuAspLeuProGluLysGlnAspGlyThrValPheProSerSerLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 snProTyrPheSerSerTrpProProSerGlyThrSerSerLysMetSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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JS AW504119
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KEYWORDS
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us-09-600-358a-4.rst

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214 ysTyrGlnGluAspAspSerValProIleCysIleHisCysSerAlaGly 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est1:AW373463
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LOCUS AW373463
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                        281
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171 g 224 t 3 others
                                                                                                                                                                 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fax: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
               Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 sAlaTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAspPheT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AGCATATGTAGCAACTCAAGGACCTTTAGCAAATACAGTAATAGATTTTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 rpArgMetIleTrpGluTyrSerValLeuIleIleValMetAlaCysMet 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 yGluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGluL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 ysArgLysSerAspTyrIleIleArgThrLeuLysValLysPheAsnSer 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pValProSerSerIleAspProIleLeuGluLeuIleTrpAspValArgC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATTCAGACTATATCAATGCAAATTTTATAAAAGGGCGTCTATGGGCCCAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 AspSerSerTyrIleAsnAlaAsnPheIleLysGlyValTyrGlyProLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 GluTyrGluMetGlyLysLysLysCysGluArgTyrTrpAlaGluProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 4
Percent Identity: 60.687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AU132040 from: 1
                                                                                        Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
                                                                         HRI human cDNA project
 (bases 1 to 811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              835.00
3.902
81.679
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US-09-600-358A-4 x AUI32040
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                                                         Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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COMMENT
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REFERENCE
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AW373463 521 bp mRNA linear EST 04-FEB-2000 RCO-BT0522-071299-011-c01 BT0522 Homo sapiens cDNA, mRNA sequence. AW373463
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2eRCO-BTO522-
071299-011-c01&t3=1999-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 22
High quality sequence start: 22
High quality sequence stop: 520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. H. (bases 1 to 521); Horgp http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                     264 rgGluMetArgThrGlnArgProSerLeuValGlnThrGlnGluGlnTyr 280
                                                                                                                                                                                                                                                                                                       597
                                                                                                                                                                                                                                                                                                                                                                                                         647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  648 ATATGAAATTCATGGAGCTCAGAAATTGCTGATGGAGTGAATTA 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 lyThrGluSerGlnAlaLySHisCysIleProGluLysAsnHisThrLeu 320
GluLeuValTyrAsnAlaValLeuGluLeuPheLysArgGlnMetAspVa 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 l......LysHisSerG 304
                                                                                                                                                   247 uLeuLysAspGlyIleIleProGluAsnPheSerValPheSerLeuIleA 264
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                                                                                                                                                                           598 GAACTTGTTCATAGAGCTATTGCCCAACTGTTTGAAAAACAGCTACAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 ACACTGAAAACATGATCAGCTCCATAGAGCCTGAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                739 ......GATTCTTCTTCTNCAAAACCACCAAGGACC 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 GlnAlaAspSerTyrSerProAsnLeuProLysSer 332
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us-09-600-358a-4.rst

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AUTHORS
TITLE
JOURNAL
COMMENT
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   REFERENCE
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into the pUC 18 vector. Reverse transcription of tissue mRNA and DNA amplification were performed under low stringency conditions." 102~c~101~g~148~t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uValAspSerLysGluAsnPheSerTyrLeuGluSerGlnProHisAspS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 spPheLeuGluLeuAsnTyrSerPheAspLysAsnAlaAspThrThrMet 396
                                                                                                                                                                                                                                                                                                                                                                                          397 LysTrpGlnThrLysAlaPheProlleValGlyGluProLeuGlnLysHi 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AAATGGCAGACAAAAGGCATTTCCAATAGTTGGGGAGCCTCTTCAGAAGCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 GGTGGACAGCAAGGAGAACTTTTCTTATTTGGAATCTCAACCACATGATT 403
                                                                                                                                                                                                                                                     347 MetGluIleLysGluSerSerSerPheAspPheArgThrSerGluIleSe
                                                                                                                                                                                                                                                                        363 rAlaLysGluGluLeuValLeuHisProAlaLysSerSerThrSerPheA
                                                                                                                                                                                                                                                                      Gaps: 1
Percent Identity: 93.064
                                                                                                                      Length:
                                                                                                                                                                                                                          to: 521
                                                                                                                                                                                                                          from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 laSerAsnValLysHis 518
                                                                                                                  824.00
4.905
97.110
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                                                                                                                                                                             alignment_block:
US-09-600-358A-4 x AW373463
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LOCUS AW363814
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                                                                                                                      Quality:
                                                                                                                                                Percent Similarity:
                                                                                                                                    Ratio:
                                           170
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                                                                                                    alignment_scores
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SOURCE
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                                                           ORIGIN
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                                                                                                                                                                                          Tal: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-RC0&t2-RC0-CT0358-071299-011-a08&t2-1999-12-07&t4-1)

Seq primer: puc 18 forward

High quality sequence start: 57

High quality sequence stop: 276.
                                                                                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 euAsnTyrSerPheAspLysAsnAlaAspThrThrMetLysTrpGlnThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 pLeuGlySerLeuLeuPheGluGlyCysSerAsnSerLysProValAsnA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 LysalaalaLysMetMetasnGlnGlnArgThrLysMet.GluIleLysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AAAGCAGCAGAAATGATGAACCAATAAAGGACAAAAATGGGGAGTCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 uLeuValLeuHisProAlaLysSerSerThrSerPheAspPheLeuGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 TAPATTACAGTTTAGACAAAATGCTGACACAACAACCATGAAATGGCAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 luSer.SerSheAspPheArgThrSerGluIleSerAlaLysGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 192
Gaps: 2
Percent Identity: 83.333
                HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AW363814 from: 1 to: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stringency conditions.
(bases 1 to 588)
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4.427
92.708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
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                                                                                                                                                                            Brazil
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (bases 1 to 745)

I. Unpublished (1999)

L. Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue procurement: DCTD/DTP

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI474 row: a column: 22

High quality sequence stop: 600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6025433B1F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4666653 5', mRNA sequence.
BG498752.1 GI:13460269
                                                                                                                                                                                                                                                                                                                                                                                                                                                  yrIleAsnAlaAsnPheIleLysGlyValTyrGlyProLysAlaTyrIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eTrpGluTyrSerValLeuIleIleValMetAlaCysMetGluTyrGluM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etGlyLysLysLysCysGluArgTyrTrpAlaGluProGlyGluMetGln 150
                                                                                                                                      34 lnSerThrLysTyrLysAlaAspLysThrTyrProThrThrValAlaGlu 50
                                                                                                                                                            166 AATCTACCAAGTACAAGGCAGACAAAATATACCTACAAACGTGGCTCAG
                                                                                                                                                                                                                                                                                                                 pTyrSerArgValGluLeuSerLeuIleThrSerAspGluAspSerSerT
                                                       sLysIleThrLysGluGluPheAlaAsnGluPheLeuLysLeuLysArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 LeuGluPheGlyProPheSerValSerCysGluAlaGlu 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 CTGCAATTTGGCCCCTTTTCTATATCCTGTGAAACTGAG 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             554 bp mRNA linear EST 25-MAY-2000
EST346970 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
RGIC218 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 554)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location = "Rattus sp."

/ Organism="Rattus sp."
/ Ob xref="taxon:10118"
/ clone="RGIC218"
/ clone="Normalized rat embryo, Bento Soares"
/ dev_stage="embryo 8, 12, 18 dpc"
/ note="Vector: pT773Pac; Site_1: EcoRI; Site_2: NotI"
/ 123 c 129 g 136 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information Seq primer: MI3 Reverse.
                                                                                                                                                                                                                                                        451 ThrProPheGluLeuIleGlnGlnArgGluThrLysGluValAspSerLy 467
                                            sGluAsnPheSerTyrLeuGluSerGlnProHisAspSerCysPheValG 484
                                                                                                                        484 luMetGlnAlaGlnLysValMetHisValSerSerAlaGluLeuAsnTyr 500
                                                                                                                                                                                                   1 MetAspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850,
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 163
Gaps: 0
Percent Identity: 86.503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        565 GCCCCATGACTCTAGTGCTCTT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW915666.1 GI:8081371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                        SHisHisAspSerSerAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.841
96.319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AW915666
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US-09-600-358A-4 x AW915666
                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est1:AW915666
                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS AW915666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene Index
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KEYWORDS
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                     465
                                                                                                   467
                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                      517
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3.421
69.079
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US-09-600-358A-4 x BI152499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          718.50
                                                                             mRNA sequence.
                   seq_documentation_block:
LOCUS B1152499
                                                                                                                                                     house mouse
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Percent Similarity:
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                                                                                             BI152499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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                                                     DEFINITION
                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                         ORGANISM
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                                                                                             ACCESSION
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KEYWORDS
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                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
       /LISBUE_LYPE="ademocrationa"
//lab_host="bildo (T1 phage resistant)"
//note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggcgcctcggcc); Site_2: Sfil (ggccattatggcc); Double-stranded CDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5' CACGCCATAATGCC-3' and 3' adaptor sequence: 5' ATTCTAGGCCAATGATGCC-3' and 3' adaptor sequence: 5' ATTCTAGGCCAAGGCGGCGCGAATGATGCC-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0,9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 ATGGACCAAAGAGAAATTCTGCAGAAGTTCCTGGATGAGGCCCAAAGCAA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 GAAAATTACTAAAGAGGAGTT.GCCAATGAATTTCTGAAGCTGAAAAGGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 AATCTACCAAGTACAAGGCAGACAAAACCTATCCTACAACTGTGGCTGAG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 AAGCCCAAGAATATCAAGAAAAACAGATATAAAGGATATTTGCCCTATGA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eTrpGluTyrSerValLeuIleIleValMetAlaCysMetGluTyrGluM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 etGlyLysLysLysCysGluArgTyrTrpAlaGluProGlyGluMetGln 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 LeuGluPheGlyProPheSerValSerCysGluAlaGluLysArgLysSe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lnSerThrLysTyrLysAlaAspLysThrTyrProThrThrValAlaGlu 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetAspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTyrSerArgValGluLeuSerLeuIleThrSerAspGluAspSerSerT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 TTATAGCCGGGTAGAACTATCCCTGATAACCTCTGATGAGGATTCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 sLysIleThrLysGluGluPheAlaAsnGluPheLeuLysLeuLysArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 TGGGAAAG......
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Percent Identity: 85.000
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145 c
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4.761
86.111
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                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                  245
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                                                                                                                                                                                                                                                                  BASE COUNT
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                                                                                                                                                                                                                                                                                      ORIGIN
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seq_name: gb_est2:BI152499

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B1152499 835 bp mRNA linear EST 05-JUL-2001 602915640F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5066337 5',
                                                                                                                                                                                                                            SM Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 835)

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov/

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

High quality sequence stop: 762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C2ECH II (feral)"
/db_xref="taxon:10090".
/clone="IMAGE:5066337"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin.
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 GAAGAGICCGGACCACAAIGGGGAGGACAACTICGCCCGGGACTICAIGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 Т..... 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 ysLeuLysArgGlnSerThrLysTyrLysAlaAspLysThrTyrProThr 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAspGlnArgGluIleLeuGlnLysPheLeuAspGluAlaGlnSerLy 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 7
Percent Identity: 49.671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .835
                                                                                                                                   BI152499.1 GI:14612500
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//note—Torgan: thymus; Vector: pT7T3D-Pac; Site_1: Not1; Site_2: PacI; 1st strand cDNA was primed with an oligo(dT) primer; double-stranded cDNA was 1gated using 5' linker ggcgctat and 3' linker actggaagcttaatt. Library size-selected >2.5 kb and average insert size is 3.5 kb. Clones were arrayed from primary plating; non-amplified. Library constructed by X. Ren and L. Stubbs (Lawrence Livermore National Laboratory and DOE Joint Genome Institute, 7000 East Ave, L-453, Livermore, CA 94550)."
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Thalsing, B., Allen, M., Bowers, Y., Person
, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
Unpublished (1999)
                                                                                                                                     Contact: Marra Mywashu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseset@atson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysAlaTyrIleAlaThrGlnGlyProLeuSerThrThrLeuLeuAspPhe 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 TrpArgMetIleTrpGluTyrSerValLeuIleIleValMetAlaCysMe 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 lygluMetGlnLeuGluPheGlyProPheSerValSerCysGluAlaGlu 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 CTICATGTTGATCACAGCCGAGTTAAGTTGACTTTGAAGACTCCATCCCA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuProTyrAspTyrSerArgValGluLeuSerLeuIleThrSerAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2802784"
/clone_lib="Ren Stubbs mouse thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 1
Percent Identity: 67.582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                        Seq primer: Primer name ambiguous
High quality sequence stop: 464.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="3 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AW822729 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                          /strain-"C3H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694.50
4.368
87.363
                                                                                                                                                                                                                                                                                                                                                                                   1. .629
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US-09-600-358A-4 x AW822729
                                                                                                                                                                                                                                                                                                          MGI:1042308
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Ratio:
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ORIGIN
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COMMENT
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      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 629)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uq17g09.yl Ren Stubbs mouse thymus Mus musculus cDNA clone IMAGE:2802784 5' similar to gb:X63440 M.musculus mRNA for PI9-protein tyrosine phosphatase (MOUSE);, mRNA sequence. AW822729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 leargGluMetArgThrGlnArgProSerLeuValGlnThrGlnGluGln 279
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                                                                               148 AAGATTCAGATTATATCAATGCAAATTTTATTAAGGGTGTGTATGGGCCA 197
                                                                                                                        LysalaTyrIlealaThrGlnGlyProLeuSerThrThrLeuLeuAspPh 113
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298 GAGAATTTGAGATGGGAAGG.
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332 GAGAAGATCCTATAACATTTGCACCATTTAAAATTTCTTGTGAAAATGAA 381

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Tue May 28

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 13-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 CysTyrGlnGluAspAspSerValProIleCysIleHisCysSerAlaGl 230
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Email: clones@txccc.org
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Schneider C, Hayashizaki Y, High efficiency selection full-length cDNA by improved biotinylated cap trapper. DNA Res 4: 1, 61-6, Feb 28, 1997)"
78 c 115 g 148 t
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US-09-600-358A-4 x BM194577
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Human Cytoplasmic phosphatase Lyp2, cDNA.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human breast and o Mouse ischaemic co cDNA encoding a no Rat protein tyrosi Human brain derive tyrosine pho Human PTP04 encodi Human Cytoplasmic Human Cytoplasmic Description Human AAV03112 AAV17097 AAV17099 AAX90695 AAV81742 AAH79342 AAF21801 AAX90696 **ABI99910** П DB Length 3058 3580 2452 1286 2983 1529 2226 2810 Query Match 1 73.4 26.4 15.6 9.2 9.1 8.6 100.0 89.0 2074.6 1729 621.4 368 216.4 214.2 202.2 Score ₩ 4 2 2 4 4 7 7 . 9 Result

Human secreted pro	Human polynucleoti	Partial PCR fragme	Human EST-derived	Human polynucleoti	Partial cDNA encod	CDNA.	Chicken protein ty	Chicken transmembr	Human protein enco	Human polynucleoti	Human polynucleoti	Human cancer agent	Tyrosine phosphata	Murine metastatic	Nucleotide sequenc	Nucleotide sequenc	Nucleotide sequenc	Human tyrosine dep	Mouse ischaemic co	Osteotesticular pr	or-t	DNA encoding novel	Human protein phos	Human protein tyro	Human polynucleoti	Human polynucleoti	Human breast cance	Rabbit osteoclast-	Human EST-derived	Rat mucocardial ce	Rat receptor type-	Human PTP-OB. Hom	Human protein tyro		Human protein tyro	
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ALIGNMENTS

Lymphoid Protein Tyrosine Phosphatase gene; Lyp gene; immunosuppressant; intracellular tyrosine phosphatase; PrPase; Iymphocyte; fetal liver; resting lymphoid cell; protein tyrosine kinase; PrKs; transgenic animal; lymphoma; T cell antigen receptor signalling; intronic sequence; cytokine receptor signalling; protein tyrosine phosphatase; PTPase; ds. /*tag= a
/*tag= a
product= "Cytoplasmic phosphatase, Lyp2"
/note= "Expressed in fetal liver tissue and resting
lymphoid cells" Location/Qualifiers WO9936548-A1 Homo sapiens

99WO-CA00038 98CA-2220853

18-JAN-1999;

16-JAN-1998;

us-09-600-358a-3.rng

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The present cDNA sequence is that of the Lymphoid Protein Tyrosine Phosphatase gene, Lyp2 that encodes a cytoplasmic tyrosine phosphatase protein with a single catalytic domain. The Lyp gene has been localised to human chromosome lpl3. It is expressed significantly in fetal liver and in resting lymphoid cells. The Lyp2 gene sequence arises by a literative splicing of the Lyp1 mRNA and the coding sequence reads into the intronic sequence of Lyp1 till a termination codon is encountered. Lyp gene products are important for regulation of T cell antigen and cytokine receptor signalling and for early and late stages of T cell ciferentiation. Lyp2 has immunosuppressive activity. This sequence is used to treat lymphoma, to reduce or prevent T cell activation or proliferation and to control thymcoyte differentiation. Fragments of this gene are used, as probes or primers, to identify allelic variations can for diagnosis of diseases associated with reduced Lyp activity. Transgenic animals in which a Lyp gene has been inactivated or replaced the activity of the control cont
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Location/Qualifiers

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The present cDNA sequence is that of the Lymphoid Protein Tyrosine Phosphatase gene, Lyp 1 that encodes a cytoplasmic tyrosine phosphatase protein with a single catalytic domain. The Lyp gene has been localised to human chromosome lpl3: It is expressed in the lymphoid cells, particularly in thymcoytes, mature B and T cells. It is involved in lymphocyte growth and development. Lyp gene products are important for regulation of T cell antigen and cytokine receptor signalling and early and late stages of T cell adifferentiation. Lyp lass immunosuppressive activity. This sequence is used to treat lymphoma, to reduce or prevent T cell activation or proliferation and to control thymocyte differentiation. Fragments of this gene are used, as probes or primers, to identify allelic variations and for diagnosis of diseases associated with reduced Lyp activity. Transgenic animals in which a Lyp gene has the lasting and inactivated or replaced by a heterologous Lyp gene are used to
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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence encodes human PTP04. The above proteins. The present sequence encodes human PTP04. The above proteins. The present sequence encodes human PTP04. The above proteins and antagonists of substances that modulate their activity (i.e. agonists and antagonists. Including MBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction or pathways that involve the proteins, particularly cancer (e.g. leukaemia and Imphoma), while modulaters of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, are serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNN, to generate transgenic animals and in generate therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                               New nucleic acid encoding specific protein tyrosine phosphatases useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease
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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are proteins AAB58711 - AAB59128. The DNA and protein sequences are sesociated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the invention are associated DNA. protein, agonist contropic, neuroprotective, antiviral; antiallergic; hepatotropic, or antagonist sequences exhibit cytoStatic; immunosuppressive; antidiabetic; antifinamatory; antiolicer; vulnerary; anticontusant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynuclectide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, proteins, agonists and agonists may also be used in the diagnosis, allergies, autoimmune thempolytic anaemia, autoimmune thyroidilis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                        Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autofimune thyroiditis; diabetes mellitus; crohn's disease; multiple sclerosis; rhemmatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
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Claim 1; Page 622; 1299pp; English.
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Query Match Best Local Similarity

BP; 410 A; 273 C; 209 G; 389 T; 5 other;

Sequence 1286

cerebral anoxia and epilepsy; and infectious diseases

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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a genes (I) in a test sample comprising genes selected from profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemia condition (e.g. compression ischaemia) or particular genes (AB199202 to AB199912, encoding expression levels of particular genes (AB19202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes are used as an indicator when screening for ischaemic condition-improving represent PCR primers for ischaemic diseases. AB199913 and AB199914

represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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Pred. No. 6.7e-87;
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Best Local Similarity 64.9%;
Matches 583; Conservative (
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P-PSDB; ABB57374
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The present sequence encodes a novel murine non-receptor protein tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein is predominantly expressed in early hematopoietic stem cells (HSCs) or progenitor cells, and lacks expression in adult tissues. The protein has a N-terminal tyrosine phosphatase domain, followed by a region rich in serine, threonine and proline and a C-terminal region of about 15-25 amino acids which is rich in basic amino acid residues. The protein is capable of tyrosine dephosphorylation in hematopoietic progenitor cells, and functional derivatives of such native tyrosine phosphatases. The phosphatase domain of the PTP HSC or a PTP HSC expressing HSC or progenitor cell can be used in an assay for the identification of PTP HSC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-receptor protein tyrosine phosphatase; hematopoietic stem cell; PTP HSC, progenitor cell; tyrosine phosphatase domain; PTP HSC agonist; tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist; stem cell differentiation; a
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antagonists or agonists. The antagonist can be used to induce the differentiation of stem cells, such as undifferentiated malignant hematopoietic cells, e.g. leukaemia cells, which may facilitate their treatment. The PTP HSC or an agonist antibody against the PTP HSC can be used for the expansion of undifferentiated stem cells in cell culture (this allows expansion of HSC prior to autologous or heterologous bone marrow transplantation), while the agonist antibody along with a hematopoietic growth factor can be used for the expansion of undifferentiated stem cells in vivo.
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Pred. No. 6.3e-47;
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/note= "GC-rich track, part of Kozak sequence"
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/transl_except= (pos:162..164, aa:His)
/transl_except= (pos:1182..1184, aa:Ser)
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protein tyrosine phosphatase; signal transduction;
therapy; diagnosis; ss.
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"site of 367 bp intron"
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"site of 80 bp intron"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This cDNA clone codes for a novel rat protein tyrosine phosphatase, designated PPP20 (see AAW49906), that regulates growth factor stimulation of cellular differentiation. The clone was isolated from a rat phaeochromocytome PC12 cDNA library by PCR amplification using primers based on consensus sequences (see AAW49915-16) of known C PTPs. The invention relates to novel proteins (see AAW49906-14) involved in cellular signal transduction and to the nucleic acids (see AAV17097-99) coding for them, and provides vectors, host cells, purified recombinant proteins, methods for identifying compounds that bind the novel proteins or abrogate their interactions with natural binding partners, as well as methods for the diagnosis and treatment of diseases associated with the novel proteins. For STP20, activators may act as anti-cancer therapeutics that stimulate cell differentiation rather than proliferation, while inhibitors may be useful for treating neural injuries by delaying the differentiation of transplanted neuronal stem cells until they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 ataacctctgatgaggattccagctacatccaatgccaacttcattaagggagtttatgga 326
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treatment of signal transduction disorders
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                                                    Protein tyrosine phosphatase; PTP20; rat; signal transduction; cell differentiation; cancer; neural injury; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen Z, Kharitonenkov AI, Kim YW, Nayler O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2226 BP; 574 A; 591 C; 604 G; 457 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                  Rat protein tyrosine phosphatase PRP20 cDNA
                                                                                                                                         Location/Qualifiers
28..1389
/*tag= a
2150..2156
/*tag= b
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96US-0019629.
96US-0023485.
96US-0030860.
96US-0030864.
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17-JUN-1996;
09-AUG-1996;
13-NOV-1996;
15-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                             phosphatase (PTP), designated brain derived phosphatase I (BDP-1, see AAW49908), that is expressed in most tissues and cell lines at basal level, but expressed high in epithelium origin cell lines and cancer cell lines. BDP-1 was originally identified in a human brain cDNA library, although the full-length clone was isolated from the haematopoletic MEG01 cDNA library. The invention relates to novel proteins (see AAW49906-14) involved in cellular signal transduction and to the nucleic ceids (see AAV17097-99) coding for them, and provides vectors, host cells, purified recombinant proteins, methods for identifying compounds that activate or
                                                                                                                                                                                                                                                                                                                           New phosphatase and kinase enzyme(s) - useful in the diagnosis and treatment of signal transduction disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibit the novel proteins, as well as methods for the diagnosis and treatment of diseases associated with the novel proteins.
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                                                                                                                                                                                                                                                                                                                                                                                     This cDNA sequence codes for a novel human protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.6%; Score 202.2; DB 19; Length
56.5%; Pred. No. 4.7e-43;
ive 0; Mismatches 303; Indels
                                                                                                                                                                                                                                                        Kharitonenkov AI, Kim YW, Nayler O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2810 BP; 700 A; 808 C; 808 G; 494 T; 0 other;
                     /*tag= f
/note= "T-rich sequence required for
polyadenylation"
                                                                                                                                                                                                                                 (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
note= "site of 91 bp intron"
                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 3a-d; 138pp; English.
                                                                                                                                                                       96US-0019629.
96US-0023485.
96US-0030860.
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           misc_feature
                                                          polyA_signal
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                                                                                                                                       17-JUN-1997;
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13-NOV-1996;
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sequence tag; secreted protein; cDNA isolation;
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                                                                          ggcttttctgcatcactctgataaaggagaagtggctgaatgaggacatcatgctcagga 566
                                                                                                                                                                                                                                                                                                                       ggccagaccatgatgtaccttcatctatagaccctattcttgagctcatctgggatgtac 678
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                                                                                                                                                                                                                                        ccctcaaggtcacattccagaaggagtcccgttctgtgtaccagctacagtatatgtcct
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cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                           Gaps
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Zhang J
                                                                                                                              Length 205;
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Yang Y,
                                                                                                                                                                                                                                                                                     121 aatttetgaagetgaaaaggeaatetaecaagtacaagge 160
                                                                                                                                                                                                                                                                                                      Score 160; DB 21;
Pred. No. 2.1e-32;
0; Mismatches 0;
                                                                                         Sequence 205 BP; 63 A; 46 C; 44 G; 52 T; 0 other
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Xu C, Xue AJ,
l, Drmanac RT;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                              AAI58418 standard; cDNA; 4798
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2000US-0552317.
2000US-0598042.
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2000US-0653450.
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2000US-0693036
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                                                                                                                                                        Matches 160; Conservative
                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAM39262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukaemia; ss
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19-OCT-2000;
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Zhao QA,
                                                                                                                              Query Match
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                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, fimunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scienosis, and Shy Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                            Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2374 tottcagtggtcccattgtggtgcactgcagtgctggtgttgggcgcacaggaacctata 2433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4798;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4798 BP; 1629 A; 850 C; 950 G; 1369 T; 0 other;
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ches 277;
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Claim 1; SEQ ID NO 621; 10078pp; English.
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RESULT

AAQ73786

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proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.
                 agaggacaacaagccagttactgtctttggagatatagtgattacaaagctaatggagga 543
                                                                                   tgttcaaatagattggactatcagggatctgaaaattgaaaggcatggggattgcatgac 603
                                                                                                                                                                                                                                                                           Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of
                                                                                                                                       tattettgageteatetgggatgtacgttgttaceaagaggatgaeagtgtteeeatatg
                                                                                                                                                                                                                         tctaattcactttgtgaagttggttcgagcaagcagggcacatgacaccaccactatgat
                                                                                                                                                                                                                                                            cattcactgcagtgctggctgtggaaggactggtgttatttgttgttgttgattatac
                                                     aaggaaatctgattatataatcaggactctaaaagttaagttcaatagtgaaactcgaac
                                                                                                                       tatctaccagtttcattacaagaattggccagaccatgatgtaccttcatctatagaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; hc tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
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Werhman T;
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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P-PSDB; AAM23689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 attagtaatgctaacacagtgttttgaaaaaggacggatcagatgccatcagtattggcc 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of a partial fragment of a new protein tyrosine phospatase PTP-S31D that was isolated from RNA from human skeletal muscle. Such DNA can be used to treat cancer and diabetes. See also AAQ73782-8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tattaatgccagctatatttctggttatttatgtccaaatgaatttattgctactcaagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - is used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New protein tyrosine phosphatase PTP-S31 - is used to deve prods. for treating or preventing disease associated with abnormal PTP-S31, e.g. cancer or diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 130.6; DB 15; Length
Pred. No. 3.8e-24;
0; Mismatches 294; Indels
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                                                                                                                                     Protein tyrosine phosphatase; cancer; diabetes; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                           /*tag= b
/note= "unknown base"
                                                                                                                                                                                                       Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moller NPH, Ullrich A;
 BP
                                                                                                   Partial PCR fragment of PTP-S31D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Fig 6; 116pp; English
AAQ73786 standard; cDNA; 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 5.5%;
al Similarity 51.1%;
307; Conservative
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                                                                   (first entry)
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1766
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                                                                                                                                                                       sapiens
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                                                                 26-JUN-1995
                                                                                                                                                                                                                                                                                                                            WO9421800-A.
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                                                                                                                  1849 gtcaaactacataaatgccagctatattgatggtttcaaagaacccaggaaatacattgc 1908
                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humtington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                 2208
                                                                                                        ggatattttgccctatgattatagccgggtagaactatccctgataacctctgatgagga 283
                                                                                                                                          284 ttccagctacatccaatgccaacttcattaagggaagtttatggacccaaggcttatattgc 343
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                                                                       caaaacctatcctacaactgtggctgagaatgccaagaatatcaagaaaaacagatataa 223
                                                     Gaps
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                                                                                                                                                                                                                                                                                       580 gtgaaactcgaact-----atctaccagtttcattacaagaattggccagaccatg
                                                     13;
                                  Length 4965;
                                                     Indels
        971 G; 1454 T; 0 other;
                                                     275;
                                  DB 22;
                                 Score 129; DB 22
Pred. No. 1.4e-23
0; Mismatches 27
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        BP; 1683 A; 857 C;
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                                 5.5%;
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                                          Local Similarity 53.2 hes 327; Conservative
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        Sequence 4965
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                                  Query Match
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                                                    Matches
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM42213) with nootropic, the encoded polypeptides (AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1850 gtcaaactacataaatgccagctatattgatggtttcaaagaacccaggaaatacattgc 1909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 ttccagctacatccaacttcattaagggagtttatggacccaaggcttatattgc
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                                                                                                                                                                                                                                                                                                                                                                                                 Qian XB,
                                                                                                                                                                                                                                                                                                                                                                                                                          Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5%; Score 129; DB 22;
53.2%; Pred. No. 1.4e-23;
iive 0; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4193; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such as central nervous system injuries
                                                           2000US-0488725.
2000US-0552317.
2000US-0598042.
                                                                                                                                           20000S-0623450.
20000S-0653450.
20000S-0662191.
20000S-0693036.
20000S-0727344.
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Best Local Similarity 53.28
Matches 327; Conservative
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P-PSDB; AAM41048.
                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                              19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
26-DEC-2000;
                                                                                      25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
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Tue May

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The present sequence encodes partial human non-receptor protein tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein is prodominantly expressed in early hematopoietic stem cells (HSCs) or progenitor cells, and lacks expression in adult tissues. The protein has a N-terminal tyrosine phosphatase domain, followed by a region rich in serine, threonine and proline and a C-terminal region of about 15-25 amino acids which is rich in basic amino acid residues. The protein is capable of tyrosine dephosphorylation in hematopoietic progenitor cells, and functional derivatives of such native tyrosine phosphatases. The progenitor cells phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or progenitor cell can be used in an assay for the identification of PTP HSC antagonists or agonists. The antagonist can be used to induce the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-receptor protein tyrosine phosphatase; hematopoietic stem cell; PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist; tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist; stem cell differentiation; ss.
2030 atactggccgtcaatggaagaggcactcgggcttttggaagagtgttgttgtaaagatct 2089
                                                                                                                                                              2150 aagaaaaagcaactggaagaggtgactcacattcagttcaccagctggccagaccacg 2209
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                                                                                                                                                                                                                                                                                                                   2270 atttetteagtggteecattgtggtgeactgeagtgetggtgttggggegeacaggaaeet 2329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Partial cDNA encoding a novel human non-receptor tyrosine phosphatase.
                                                                                                                                                                                                                                                                                Hematopoietic stem cell non-receptor protein tyrosine phosphatase - useful for expansion of undifferentiated stem cells in cell culture
                                                                                          ---gattatataatcaggactctaaaagttaagttcaata
                                                                                                                           580 gtgaaactcgaact-----atctaccagtttcattacaagaattggccagaccatg
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P-PSDB; AAW37255.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-1997; .
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differentiation of stem cells, such as undifferentiated malignant hematopoietic cells, e.g. leukaemia cells, which may facilitate their treatment. The PTP HSC or an agonist antibody against the PTP HSC can bused for the expansion of undifferentiated stem cells in cell culture (this allows expansion of HSC prior to autologous or heterologous bone marrow transplantation), while the agonist antibody along with a hematopoietic growth factor can be used for the expansion of undifferentiated stem cells in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 tatccctgataacctctgatgaggattccagctacatcaatgccaacttcattaagggag 318
                                                                                                                                                                                                                                                                                                                                                                                                                  tttatggacccaaggcttatattgccacccagggtcctttatctacacaccctcctggact 378
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                                                                                                                                                                           Sequence 466 BP; 103 A; 122 C; 158 G; 83 T; 0 other;
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62.8%; Pred. No. 1.2e-21;
11ve 0; Mismatches 110;
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Matches 186; Conservative
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Search completed: May 26, 2002, 10:42:07 Job time: 9679 sec

Appli Appli

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Sequence 3, A Sequence 3, A Sequence 3, A Sequence 3, A Sequence 8, A Sequence 8, A Sequence 2, A Sequence 2, A Sequence 1, A Sequence 2, A Sequence 3, A Se
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Sequence 8,
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Sequence 2, Application US/09081345

Sequence 2, Application US/09081345

Patent No. 6228641

GENERAL INFORMATION:

APPLICANT: Bahija Jallal

APPLICANT: Gregory D. Plowman

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

CORRESPONDENCES: 18

CORRESPONDENCE ADDRESS:
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US-08-991-258A-3
US-08-769-399-3
US-08-91-935A-3
US-08-149-644-8
US-08-105-986A-2
US-08-105-986A-2
US-08-241-853-2
US-08-205-939-12
US-08-205-939-12
US-08-015-973-1
US-08-015-973-1
US-08-018-929-2
US-08-018-929-2
US-08-018-929-2
US-08-018-929-2
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US-08-018-929-12
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIF: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRASESO for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,345
FILING DATE: HEREWITH
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: May 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
STRANDEDNESS: single
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      ; MOLECULE TYPE: peptide US-09-081-345-2
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-081-345-18
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US-08-821-278A-18
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US-08-951-260A-7
US-08-951-260A-7
US-08-951-260A-7
US-08-91-278A-2
US-08-821-278A-2
US-08-821-278A-2
US-08-821-278A-2
US-08-685-992-22
US-08-087-244A-2
US-08-087-244A-2
US-08-087-244A-2
US-08-087-244A-2
US-08-081-258-6
US-08-08-18-5
US-08-12-58
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq length: 2000000000
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Total number of

Database

Searched:

Perfect score:

Sequence:

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Run on:

Scoring table:

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Query Match
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             Gaps
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                                                 1 MDQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAEKPKNIKKNRY
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             Indels
 Pred. No. 3e-291;
); Mismatches 3;
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APPLICANT: Bahija Jallal
APPLICANT: Brain Jallal
APPLICANT: Gregory D. Plowman
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: PPP04 RELATED DISORDERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: storage
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Sequence 18, Application US/09081345
Patent No. 6228641
99.48;
            Conservative
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California
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 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 RISEISAKEELVLHPAKSSTSFDFLELNYSFDKNADTIMKWQTKAFPIVGEPLQKHQSLD 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 NHLGREIQAQCSIPEQSLIVVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 VDYTWMLLKDGIIPKNFSVFNLIQEMRTQRPSLVQTQEQYELVYSAVLELFKRHMDVISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 KHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQ----QRTKMEIKESSSFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNQESAVLATAPRIDDEIPPPLPVRTPESFIVVEEAGEFSPNVPKSLSSAVKVKIGTSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETRIIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFSSWPPSGTSSKMSLDLPEKQDGTVFPSSLLPTSSTSLFSYYNSHSSLSLNSPTNISSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDQREILQQLLKEAQKKKLNSEEFASEFLKLKRQSTXYKADKIYPTTVAQRPKNIKKNRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDSCFV-EMQAQKVMHVSSAELNYSLPYDSKHQIRNASNVKHHDSSALGVYSYIPLVENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 8.5e-191;
66; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.2%; Score 2356.5;
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,345
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: May 20, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 334/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 802 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 68.5
Matches 474; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
7 TOPOLOGY: linear
9 MOLECULE TYPE: peptide
US-09-081-345-18
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24 FANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSS 83
                                                                                                                                                                                           144 AEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID
                                                                                                                                                                                                                                                                    204 PILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLI
     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN TITLE OF INVENTION: TYROSINE PHOSPHATASES CORRESCENDENCES: 36
CORRESCENDENCE ADDRESS: ADDRESSE: HAMILTON, BROOK, SMITH & REYNOLDS, STREET: Two Militia Drive CITY: Lexington STATE: MA
   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7%; Score 928.5; DB 2;
65.7%; Pred. No. 9.4e-71;
tive 41; Mismatches 43
     Mismatches
                                                                                                                                                                                                                                                                                                                                             264 REMRTQRPSLVQTQEQYELVYNAVLELFKROM 295
                                                                                                                                                                                                                                                                                                                                                                   240 QEMRTQRHSAVQTKEQYELVHRAIAQLFEKQL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.7%
Best Local Similarity 65.7%
Matches 167; Conservative
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-685-992-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            us-08-685-992-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 YINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYW 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 AEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 FANEFLKIKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 PILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
APPLICANT: Lasky, Laurence A.
TILLE OF INVENTION: Protein Tyrosine Phosphatases
FILE REFERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                               APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: Protein Tyrosine Phosphatases
FILE REFERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.2%; Score 1345.5; DB 4
88.5%; Pred. No. 5.6e-106;
live 18; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 REMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 QEMRTQRPSLVQTQEQYELVYSAVLELFKRHMDVISDNH 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1008.5; DB 4
Pred. No. 1.8e-77;
                                                         657 WGGTSEPKKFDDSVILRPSKSVKLRSPKSGKN 688
                                                                               Sequence 18, Application US/08821278A Patent No. 6238902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08821278A Patent No. 6238902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.9%; 65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapien
US-08-821-278A-19
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                    RESULT 3
US-08-821-278A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-821-278A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-821-278A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 19
LENGTH: 272
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LENGTH: 278
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Gaps

us-09-600-358a-4.rai

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44 YPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQ 103
                                                                               104 GPLSTTLLDFWRMIWEYSVLIIVWACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAE 163
                                                                                                    62 GPLANTVIDFWRMVWEYNVVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCEDE 121
                                                                                                                                                                                   2 YPTATGEKEENVKKNRYKDILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQ
                                                                                                                                                              164 KRKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPI
                                                                                                                                                                                                                                          224 CIHCSAGCGRIGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: AOK1, NaOhito
APPLICANT: Ullitch, Axel
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.7%; Score 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESD for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,260A
FILING DATE: October 16, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/1897/00946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,860
FILING DATE: No. 6004791ember 13,
APPLICATION NUMBER: PCT/1897/0094
FILING DATE: June 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: WAIDLEY, RICHARD J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08951260A Patent No. 6004791 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 227,
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISICS:
LENGTH: 453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                     : |: :||::|: :
239 HRAIAQLFEKQLQL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                            284 YNAVLELFKROMDV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-951-260A-7
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                                                                                                                                                                                                    44 YPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQ 103
                                                                                                104 GPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAE 163
                                                                                                                     62 GPLANIVIDEWRAVWEXNVVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCEDE 121
                                                                                                                                                                               164 KRKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPI 223
                                                                                                                                                                                                                                                            224 CIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELV 283
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 253;
                                                                                                                                                                                                                                                                                                                                                                                       us-U9-144-925-20
Sequence 20, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: TONKS, Nicholas
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: HAMILTON, BROOK, SMITH & REXNOLDS, P.C. STREET: Two Milltia Drive
CITY: Lexington
STREET: MA
COUNTRY: USA
ZIP. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSHL96-03Z
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APPLICATION NUMBER: 08/685,99;
FILING DATE: July 25, 1996
ATTORREY/AGENT IRFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFRENCE/DOCKET NUMBER: CSHLS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 65.7<sup>3</sup>
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-09-144-925-20
                                                                                                                                                                                                                                                                                                                                                                         : |: :||::|:
239 HRAIAQLFEKQLQL 252
                                                                                                                                                                                                                                                                                                                                               284 YNAVLELFKROMDV 297
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CLASSIFICATION:
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US-09-144-925-20
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66 YDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLII 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 QSKKITKEEFANEFLKLKRQST----KYKADK----TYPTTVAENAKNIKKNRYKDILP 65
                                                                                    Sequence 2, Application US/08854585
Patent No. 6114140
GENERAL INFORMATION:
APPLICANT: TORAS, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 TIYQFHYKNWPDHDVPSSIDPILELIWDVRCY--QEDDSVPICIHCSAGCGRTGVICAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1337;
                                                                                                                                                                                                              E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.1%; Score 50%; DB 3; L
.llarity 38.3%; Pred. No. 5.1e-34;
Conservative 51; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27866/31954
                                                                                                                                                                                                                                    STREET: 233 South Wacker Drive, St
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA: US/08/854,585
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/237,940
   301 PHYQNLKENCAPICKEAFSLRTSSALP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9505512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 276
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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Best Local Similarity
Matches 113; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                           ZIP: 60606
                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
PCT-US95-05512-2
                                                                         US-08-854-585-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 DVVPYDETRVILSLLQEEGHGDYINANFIRGTDGSQAYIATQGPLPHTLLDFWRLVWEFG 123
                                                                                                                                                                                                  VLIIVWACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKR-KSDYIIRTLKVKFNS 180
                                                                                                                                                                                                                     ETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGGGRTGVICAI 240
                                                                                                                                                                                                                                                                                          VDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD---- 296
                                                                                                                                                                                                                                                                                                                                                                   64 LPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVD 242
                                                                                                                           62 DILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYS 121
                    Gaps
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                                                                                      4 QSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAWKTEGVCSTKAGSQQGNSKKNRYK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 EILQKFLDEAQSKKITKEE-FANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDI 63
                                                      3 QREILQKFLDEAQSKKITKEE-FANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                      -----VIRDKHSGTESQAKHCIPEKNHTLQADSYS-----PNLPKSTTKA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                             302 LYQNLKENRAPICKDSSSLRTSSA---LPATSRPLGGVLRSISVPGPPTLPMADTYA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
 ; Pred. No. 4.5e-55;
58; Mismatches 117; Indels
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APPLICANT: Lasky, Laurence A.

TITLE OF INVENTION:
FILE REPERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
FILE OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.4%; Score 736.5; DB 4 44.0%; Pred. No. 4.2e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08821278A Patent No. 6238902
43.18;
                  Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Mus Musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-821-278A-2
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45 PTTVAENAK -- NIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIAT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 QGPLPNTIADFWRWWENRCRIIVMLSRESEGSENCRIKCDRYWPEQIGGEQFSIYGNGN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 LEFGPFSVSCEAEKRKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSIDPILELIW
           HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 IIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVL-ELFKR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 ----DFNLFSIVLKLREQRPGMVQQLEQYLFCYKTILDEIYHR 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 DVRCYQ-----EDDSVPICIHCSAGCGRTGVICAIV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSPEE: HAMILTON, BROOK, SMITH & REYNOLDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.6%; Score 492.5; DB 2
Best Local Similarity 38.2%; Pred. No. 8.6e-34;
Matches 108; Conservative 40; Mismatches 92
                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09144925 Patent No. 5951979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CS
TELECOMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                             Two Militia Drive
                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                        STREET: TWO ...
                                                                                              USA
                                                                                                                                                             MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 TIYQFHYKNWPDHDVPSSIDPILELIWDVRCY--QEDDSVPICIHCSAGCGRTGVICAIV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 YDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLII 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 VMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVK--FNSETR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 QSKKITKEEFANEFLKLKRQST----KYKRADK----TYPTTVAENAKNIKKNRYKDILP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1254 RLIXQIENENTV----DVYGIVYDLRMHRPLANQCTEDQYVFLNQCVLDIVRSQKD 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 DYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.1%; Score 508; DB 5; Length 1337;
Best Local Similarity 38.3%; Pred. No. 5.1e-34;
Matches 113; Conservative 51; Mismatches 111; Indels 2
                    APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-685-992-22
; Sequence 22, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
                                                                                                                                                                    233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BOTUN, MICHAEL F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
TELEPONNUNICATION INFORMATION:
TELEPAX: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein
PCT-US95-05512-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                          90909
                                                                                                                                                                           STREET:
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Length 277; Indels

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CORRESPONDENCE ADDRESS:
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                                                              STATE: New York COUNTRY: U.S.A.
                                                New York
                                                                                             10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-449-644-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 QGPLSTTLLDFWRMIWEYSVLIIVWACMEYEMGKK---KCERYWAEP------GEMQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 PTTVAENAK--NIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 DVRCYQ------DDDSVPICIHCSAGCGRTGVICAIV-------DYTWMLLKDG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08449644
Patent No. 5856162
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Ulrich, Axel
APPLICANT: Vogel, Wolfgang
APPLICANT: Wolf, Miniam
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-KAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 IIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVL-ELFKR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.6%; Score 492.5; DB 38.2%; Pred. No. 8.6e-34; tive 40; Mismatches 92
                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
FILING DATE: July 25, 1996
ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                               22:
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 38.2
Matches 108; Conservative
                           ZIP: 02421-4799
COMPUTER REDABLE FORM:
MEDIUM TYPE: Dieber
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
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                 Lexington
                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-144-925-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-449-644-2
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1170 SSHLKDEFQTLNSVTPRLQAEDCSIACLP-RNHDKNRFMDMLPPDRCLPFLITIDGESSN 1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 DSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 RYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIR--TLKVKFNSETRTIYQFHYKNWPDHDV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 DKHSGTESQAKH-------CIPEKNHTLQ--ADSYSPN--LPKSTTKAAKMMN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 KEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 PSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 VFSLIREMRTQRPSLVQTQEQYELVYNAVLEL------FK-RQMDVIR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1439;
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                                                                                                                                                                                                                                             OPERATING SYSTEM: FC-LUCS/MS-LUCS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,644
FILING DATE: 24-MAY-1995
CLASSIEICATION: 514
PRIOR APPLICATION STA:
APPLICATION NUMBER: US 08/087,244
FILING DATE: 01-JUL-1993
ATTONNEY/AGENT INFORMATION:
NAME: COTAZI, LAURA A.
REGISTRATION NUMBER: 36/72
FELECOMMUNICATION NUMBER: 36/72
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEFAX: 212-869-8864/9741
TELEFAX: SEQUENCE CHARACTERISTICS:
LENGTH: 1439 amino acids
LENGTH: 1439 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.6%; Score 492.5; 29.1%; Pred. No. 1.2
E: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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1229 YINAALMDSYRQPAAF-----IVTQYPLPNTVKDFWRLVYDYGCTSIVMLNEV 1276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 QSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
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                                                                                                                                                                                                               1:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08202389
Patent No. 5515636
GENERAL INFORMATION:
APPLICANT: Plutzky, Jorge
APPLICANT: Plutzky, Jorge
APPLICANT: Neel, Benjamin G.
APPLICANT: PROSCHOBERJ ROBERT D.
TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                              389 DKNADTTMKWQTKAF----PIVGEPLQKHQSLDLGSLLFEGCSNSKP 431
                  342 QQRTKM--EIKESSSFDFRTSEISAKEELVLHPAKSSTSFDFLELNYSF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,389
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION NUMBER: US 07/829,141
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERNCE/DOCKET NUBER: B1H92-05MA
TELECOMMUNICATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-202-389-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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1110 IYNCVKALRSRRINMVQTEEQYIFIHDAILEACLCGETAIPVCEFKAAYFDMIRIDSQTN 1169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 PSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFS 258
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                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE TITLE OF INVENTION: PHOSPHATASE-KAPPA NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,244A
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: PENNIE & EDMONDS
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 763-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                         Sequence 2, Application US/08087244A Patent No. 5863755 GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
                                                                                                                                                   Schlessinger, Joseph
                                                                                                                                                                                                                   APPLICANT: Ullrich, Axel APPLICANT: Vogel, Wolfgang APPLICANT: Fuchs, Miriam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1439 amino acids
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Ullrich, Axel
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: U.S.A.
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us-09-600-358a-4.rai

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qq	351	351 TREVEKGRNKCVPYWPEVG-MQRAYGPYSVTNVGEHDTTEYKLRTLQVSPLDNGDLIREI 409
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q	410	410 WHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVI 466
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Search completed: May 26, 2002, 12:17:53 Job time: 6148 sec

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Protein tyrosine p
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Human receptor-typ
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SHP-1 b59A mutant
SHP-1 b79A mutant
SHP-1 b79A mutant
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   Mutant mouse PTP-P
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Human protein tyro
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AAG78283
AAR63632
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AAY29591
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AAB59237
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AAM79159
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1 MDQREILQKFLDEAQSKKIT.....RPSKSVKLRSPKSGKNFSWL
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                               747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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rotal number of

Database

Searched:

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

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AAY28653

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		tion	Cytoplasm	Cytoplasmi	PTP04. HC	Human tyrosine pho	Cytoplasn	PTP-PEST (protein ty	PTP-PEST n	PTP-PEST n	mutant PTI	protein ty
		Description	Human	Human	Human	Human	Murine	Human	Human	Human	Human	Human	Mouse
		ID	AAY28653	AAY28652	AAW89247	AAG78623	AAY28654	AAM51205	AAY 67252	AAM51201	AAM51202	AAY67253	AAY67250
		. 6	20	20	20	22	20	22	21	22	22	21	21
		ength 1	692	808	807	199	802	780	780	780	780	780	775
æ	Query	Match Length DB	100.0	98.8	98.0	82.2	65.2	32.0	32.0	31.8	31.8	31.7	31.2
		Score	3615	3573	3543.5	2971,5	2356.5	1158	1157	1150	1148	1147	1127.5
	Result	No.		7	e	Ą	2	9	7	80	6	10	11

W09936548-A1

22-JUL-1999

AAY28653 standard; Protein; 692 AA. AAY28653; 01-OCT-1999 (first entry) Human Cytoplasmic phosphatase, Lyp2 protein. Lymphoid Protein Tyrosine Phosphatase; Lyp protein; immunosuppressa intracellular tyrosine Phosphatase; Presser, Fetal liver; transplant resting lymphoid cell; protein tyrosine kinase; PrKs; lymphocyte; T cell antigen receptor signalling; cytokine receptor signalling; autoimmune disease; intronic sequence; alternative mRNA splicing. Homo sapiens. Key 27.289 27.
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phosphatase

photyrosine

suppressant;

ransplant;

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/note= "Sequence rich in Pro, Glu or Asp, Ser and Thr" 741..745
/note= "Consensus sequence recognised by p34cdc2 kinase" 768..772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469..472
/label- NXXY_motif
/note= "Unique sequence recognised by phosphotyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Single catalytic protein tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intracellular tyrosine phosphatase; PrPase; lymphocyte; thymocyte; r cell; B cell; protein tyrosine kinase; PTKs; immunosuppressant; T cell antigen receptor signalling; cytokine receptor signalling; autoimmune disease; transplant.
                                                                                                                                                                                     Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell;
                     CFVEMQAQKVMHVSSAELNYSLPYDSKHQIRNASNVKHHDSSALGVYSYIPLVENPYFSS
                                           WPPSGTSSKMSLDLPEKQDGTVFPSSLLPTSSTSLFSYYNSHSSLSLNSPTNISSLLNQE
                                                                                                                           /label= SH3_binding_site
/note= "Proline rich sequence"
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615.62 St3. binding site
/note- "Proline rich sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Cytoplasmic phosphatase, Lyp1 protein.
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                                                                                                                                                                                                                                                                        SEPKKFDDSVILRPSKSVKLRSPKSGKNFSWL 692
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/label- PTPase_domain
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                     99WO-CA00038
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The present protein sequence is that of the cytoplasmic, Lymphoid Protein Tyrosine Phosphatase Lypl, that has a single catalytic domain. The non-catalytic portion of the phosphatase contains unique sequences, including a single PEST sequence rich in Pro, Glu or Asp, Ser and Thr. Lypl is expressed in the lymphoid cells, particularly in thymocytes, mature B and T cells and expression is increased upon activation. It is involved in lymphocyte growth and development and is phosphorylated in a cell cycle dependent manner. Lypl shares about 70% phosphorylated in a cell cycle dependent manner. Lypl shares about 70% sequence identity with the murine phosphatase Z70PEP. Lyp proteins are important for regulation of T cell antigen and cytokine receptor signalling and for early and late stages of T cell differentiation. Lypl has immunosuppressive activity. Compounds that increase expression of the protein can be used as immunosuppressive agents to reduce or prevent T cell activation or proliferation, to control thymocyte differentiation can denote the control thymocyte of the control manner of the control manner situations.
                                                                                                                                   New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signalling through T cells, particularly as immunosuppressant
                                                                                                                                                                                                                                                  Claim 4a; Page 53; 105pp; English
                                                      WPI; 1999-444404/37.
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  Length 808;
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98.8%; Score 3573; DB 20; 100.0%; Pred. No. 4.1e-296; tive 0; Mismatches 0;
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PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease;
SAVLATAPRIDDEIPPPLPVRTPESFIVVEEAGEFSPNVPKSLSSAVKVKIGTSLEWGGT
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                                 sepkkfddsvilrpsksvklrspks 685
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970S-0044428.
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970S-0049477.
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SA, Hui TH, Plowman GD Clary D, Courtneidge S), Onrust S, Peles E, WPI; 1999-009434/01. N-PSDB; AAV81742. Ď, App H, Markby

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(SUGE-) SUGEN INC.

New nucleic acid encoding specific protein tyrosine phosphatases useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease

Claim 2; Page 151-153; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents human PTP04. The above proteins. The present sequence represents human PTP04. The above proteins. The present sequence represents human PTP04. The above proteins, other than 12.0 min tyros in in vitro. These substances are used to identify substances that modulate their activity (i.e. agonists and antagonists, including MBP) in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and Imphoma), while modulators of ALK-7 (which is a type I receptor particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynuclectides encoding the protein can be used as probes to identify and clone related sequences; to detect protein-encoded RNN; to generate transgenic animals and in the content protein can be used to promote transgenic animals and in the content protein can be used to protein can be used to generate transgenic animals and in

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     Length 807;
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    Score 3543.5; DB 2
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   Query Match 98.0%;
Best Local Similarity 99.4%;
Matches 681; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    Human tyrosine phosphatase
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                                                                                                                                                                                                                                                                                    82.2%; Score 2971.5; DB 22.87.3%; Pred. No. 1e-244; ive 17; Mismatches 61;
                         (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP
                                                                                                                                                       Claim 4; Page 12-13(Disclosure); 29pp; Chinese
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                                                                                                                                                                                                                                                            /note= "Catalytic protein tyrosine phosphatase domain"
                                                                                                                     Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell; intracellular tyrosine phosphatase; PTPase; lymphocyte; murine; protein tyrosine kinase; PTKs; immunosuppressant; PEST sequence; T cell antiqen receptor signalling; autoimmune disease; transplant; cytokine receptor signalling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signalling through T cells, particularly as immunosuppressant
                                                                                                Murine Cytoplasmic phosphatase, Z70PEP protein.
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/label= SH3_binding_site
/note= "Proline rich sequence"
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27..288
                     AAY28654 standard; Protein; 802 AA.
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65.2%; Score 2356.5; DB 20; Length 802; 68.5%; Pred. No. 3.9e-192; Live 66; Mismatches 139; Indels 13;

Best Local Similarity 68.5 Matches 474; Conservative

Query Match

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PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide; dephosphorylation; phosphotyrosine; human; PTP-PEST.
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                                                                  121 SVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNS
                                                                                                                          61 KDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEY
                                                                                                                                                                 ETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAI
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MDQREILQKFLDEAQSKKITKEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRY
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                                                                                                                                                     between a protein tyrosine phosphatase (PTP) and a tyrosine phosphatase phosphorylated polypeptide using fluorescence energy signals. The methods are useful for performing screening assay to identify agents that alter PTP binding to and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence is not given in the specification but is that of human PTP-PEST protein sequence taken from Genbank (Accession Number; xP034191). The present sequence was used to generate mutants D199A (AAM51201) and C231S (AAM51202) as described in the specification.
                                                                                                                                                                                                                                                                          Note: An alternative sequence for human PTP-PEST is given in figure 1 of the specification (AAG78281).
                                                                                                                                            The invention relates to identifying agents which alter the interaction
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                                                              Screening assays to identify agents that alter protein tyrosine phosphatase (PTP) binding to, and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates -
                                                                                                                                                                                                                                                                                                                                                     32.0%; Score 1158; DB 22; Length 780; 37.2%; Pred. No. 1e-89; Live 111; Mismatches 237; Indels 144;
                                                                                                                 Example 1; Page -; 79pp; English.
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                                      WPI; 2001-570570/64.
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Best Local Similarity
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This is the amino acid sequence of human protein tyrosine phosphatase (PTP) PEST. PTP-PEST is a soluble PTP that is ublquitously expressed throughout embryonic development and in mutine adult tissues. The N-terminal portion of the enzyme encodes for the catalytic domain, while
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                                                                                                 989
                             Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion; cell migration; division; cytostatic; antiinflammatory; anglogenesis; cancer; enzyme substrate identification; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein tyrosine phosphatase (PTP) PEST amino acid sequence.
                                                                                                 632 AGEFSPNVPKSLSSAVKVKIGTSLEWG----GTSEPKKFDDSVILRPSKSVKLRSPKSG
FSYYNSHSSLSLNSPINISSLLNQESAVLATAPR----IDDEIPPPLPVRIPESFIVVEE
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/label= Pro_1
"ante= "Proline rich domain 1"
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/note= "Proline rich domain 4"
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/note= "Proline rich domain
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/note= "Proline rich domain
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/note= "Proline r.
674.680
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98US-0111993
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the C-terminal portion is composed of 5 proline rich domains, and a binding site for the adaptor protein Shc. The pro 2 domain is required for paxillin binding, and the synthesis of mutant PTP-PEST have shown comparation for paxillin binding activity. The comparation relates to a compound that is capable of interfering with the binding of PTP-PEST to signalling molecules that are involved in cell captares to a compound that is capable of interfering with the binding of PTP-PEST to signalling molecules that are involved in cell captares to a method for finding a genuine substrate for an enzyme in a comparation of PTP-PEST (see AAV67251 and AAV67253) is used in this method. The compounds have cytostatic and antiinflammatory activity. The compounds are used for making medicaments for treating a disease related compounds are used for making medicaments for treating a disease related computed and are used for making medicaments for treating a disease related computed in a compute state of the novel method is used for identifying a genuine computed is an enzyme.
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25; 296 466 462 57 KNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATOGPLSTTLLDFWRM 116 120 117 IWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKV 176 V-----IRD--KHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQQRTK 346 350 387 351 eeilgppephpvppiltpsppsafptvttvwgdndryhpkpvlhmvsseghsadlnrnys 410 632 AGEFSPNVPKSLSSAVKVKIGTSLEWG----GTSEPKKFDDSVILRPSKSVKLRSPKSG 686 MDQREILQKFLDEAQSKKIT----KEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIK KFNSETRIIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGGGRTGV ICAIVDYTWALLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 300 lyeihgaqkiadgvneintenmissiepekq----dspppkpprtrs----clvegdak 347 MEIKE-----SSSFDFRTSEISAKEEL----VLHPAKSSTSFDFLELNYS ---C---SNSKP-----VNAAGRYFNSKVPITRTKS-----TPFELIQQRETK----aspciadkisk pqelss dlnvg dts qns cvdcs vtqsnkvs vtppees qns dtpprpdrlag problem to the statement of the st463 EVDSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNY----SLPYDSKHQIRNASNV pldekghvtwsfhgpena----ipipdlsegnssdinyqtrktvsltpspttqvetpdlv 517 KHHDSSALGVYSYIPLVENPYFSSWPPSGTSSKMSLDLPEK-QDGTVFPSSLLPTSSTSL 583 dhdnts-----plfrtplsftnplhsdds----dsdernsdgavtgnktnistasat 576 FSYYNSHSSLSLNSPTNISSLLNQESAVLATAPR----IDDEIPPPLPVRTPESFIVVEE vsaatstesistrkvlpmsiarhniagtthsgaekdvdvsedsppplpertpesfvlase ----FDKNADTTMKWQTKAFPIVGEPLQKHQSLDLGSLLFEG-----Query Match
32.0%; Score 1157; DB 21; Length 7
Best Local Similarity 37.2%; Pred. No. 1.3e-89;
Matches 291; Conservative 111; Mismatches 237; Indels 177 426 237 467 g 셤 ð q ò g ŏ ò g õ qq ò g ò g à g à 8 ò g ò ç

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying agents which alter the interaction between a protein tyrosine phosphatase (PTP) and a tyrosine phosphorylated polypeptide using fluorescence energy signals. The method are useful for performing screening assay to identify agents that alter PTP binding to and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence is that of a human PTP-PEST D199A mutant.
                                                                                                                                                                                                                                                               PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide; dephosphorylation; phosphotyrosine; human; PTP-PEST; mutein; mutant.
KNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRM 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDQREILQKFLDEAQSKKIT----KEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening assays to identify agents that alter protein tyrosine phosphatase (PTP) binding to, and PTP-mediated catalytic
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Conservative 111; Mismatches 2
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Misc-difference 199
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                   IWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKV
                                                      KFNSETRIIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGV
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/note= "Wild-type Cys substituted by a
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The invention relates to identifying agents which alter the interaction between a protein tyrosine phosphatase (PTP) and a tyrosine phosphorylated polypeptide using fluorescence energy signals. The methods are useful for performing screening assay to identify agents that alter PTP binding to and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence is that of a human PTP-PEST C231S mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence is not given in the specification but is defined the wildtype human PTP-PEST sequence (AAAB21265) from Genebank (Accession Number; XPO134191). An alternative sequence for human PTP-PEST is given in figure 1 of the specification (AAG78281).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.8%; Score 1148; DB 22; Best Local Similarity 37.0%; Pred. No. 7.4e-89; Matches 290; Conservative 111; Mismatches 238;
                                                                                                                                                                                                                                                                                                   Example 1; Page -; 79pp; English
2001WO-US05180
                                        14-FEB-2000; 2000US-0181769.
                                                                                                                                                                    WPI; 2001-570570/64.
                                                                                                                              Cool DE;
                                                                                    (CEPT-) CEPTYR INC
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13-FEB-2001;
                                                                                                                            Flint AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of human (C231S) mutant protein tyrosine phosphatase (PTP) PEST. The wild-type cysteine residue at position 231 is replaced with a serine residue. PTP-PEST is a soluble PTP that is ubiquitously expressed throughout embryonic development and in murine adult tissues. The N-terminal portion of the enzyme encodes for the catalytic domain, while the C-terminal portion is composed of 5 proline rich domains, and a binding site for the adaptor protein Shc. The pro 2 domain is required for paxillin binding, and the synthesis of mutant PTP-PEST have shown that proline 362 is important for paxillin binding activity. The invention relates to a compound that is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel therapeutic agents for treating diseases which are related to cell proliferation, migration, inflammation and angiogenesis especially
                                                                                                                                             989
                                                                                                                                                                                                                                                                                                                                                                          Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion; cell migration; division; cytostatic; antiinflammatory; angiogenesis; cancer; enzyme substrate identification; mutein; human.
                                                                                                            EVDSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNY----SLPYDSKHQIRNASNV
                       pldekghvtwsfhgpena----ipipdlsegnssdinyqtrktvsltpspttqvetpdlv
                                               517 KHHDSSALGVYSYIPLVENPYFSSWPPSGTSSKMSLDLPEK-QDGTVFPSSLLPTSSTSL
                                                                    583 dhdnts-----plfrtplsftnplhsdds----dsdernsdgavtgnktnistasat
                                                                                             FSYYNSHSSLSLNSPINISSLLNQESAVLATAPR----IDDEIPPPLPVRTPESFIVVEE
                                                                                                                                           632 AGEFSPNVPKSLSSAVKVKIGTSLEWG-----GTSEPKKFDDSVILRPSKSVKLRSPKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Cys has been replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charest
                                                                                                                                                                                                                                                                                                                                                     Human mutant PTP-PEST (C231S) amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                             AAY67253 standard; protein; 780 AA.
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98US-0111993
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11-DEC-1998;
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interfering with the binding of PTP-PEST to signalling molecules that be envolved in cell migration, adhesion or division. The compound can be derived from minimal sequences found in binding sites of PTP-PEST. The invention also relates to a method for finding a genuine substrate for an enzyme in a cell that normally expresses the wild type form of the enzyme. A mutent version of PTP-PEST (represented by this sequence) is used in this method. The compounds have cytostatic and antinflammatory activity. The compounds are used for making medicaments for treating a disease related with cell proliferation, migration, inflammation and angiogenesis, especially cancer. The novel method is used for identifying a genuine substrate for an enzyme. Note: The present sequence is not shown in the specification but it has been derived from the PTP-PEST sequence (see AAV67252) shown in figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V-----IRD--KHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQQRTK 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDQREILQKFLDEAQSKKIT----KEEFANEFLKLKRQSTKYKADKTYPTTVAENAKNIK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 MEIKE-----VLHPAKSSTSFDFLTSEISAKEEL----VLHPAKSSTSFDFLELNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 kstelpgknestiegidkklernlsfeikkvplgegp----ksfdgntllnrghaikiks
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llarity 37.0%; Pred. No. 9e-89;
Conservative 111; Mismatches 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel therapeutic agents for treating diseases which are related to cell proliferation, migration, inflammation and angiogenesis especially cancer -
                                                                                                                                                                                                                                                    Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion; cell migration; division; cytostatic; antiinflammatory; anglogenesis; cancer; enzyme substrate identification; mouse.
                                                                                                                                                                                                                         Mouse protein tyrosine phosphatase (PTP) PEST amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Pro_3
/note= "Proline rich domain 3"
675..681
/label= Pro_4
/note= "Proline rich domain 4"
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/note= "Proline rich domain 1"
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/note= "Proline rich domain 5"
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355..364
/label- Pro_2
/~~te- "Proline rich domain 2'
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                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 332..339
                                                                                                                        AAY67250 standard; protein; 775 AA.
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                                 131 1hy 733
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               689
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                                                                                                                                                        AAY67250;
             687 KNF
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                                                                                                           AAY67250
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                                                                                             RESULT
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cell that normally expresses the wild type form of the enzyme. A mutant version of PTP-PBST (see AAY67251 and AAY67251) is used in this method. The compounds have cytostatic and antiinflammatory activity. The compounds are used for making medicaments for treating a disease related with cell proliferation, migration, inflammation and angiogenesis, especially cancer. The novel method is used for identifying a genuine substrate for an enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 sseesgsnshtpprpdc---lpldkkghvt----wslhgpenatpvpdspdgkspdnhs 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------trnktsistasat-vspassaesachrrv 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                KNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KENSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 lyeihgaqkiadgneittgtmyssidse----kqdspppkpprtrs----clvegdakee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 IKE------SSSFDFRTS------EISAKEELVLHPAKSSTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFLELNYSFDKNADTTMKW--------QTKAFPIVGEPLQK-HQSLDLGSLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGCSNSKPVNAAGRYFNSKVPITRTKSTPFEL-----IQQRETKEV-----
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                                                                                                                                                                                                                                                                                                     DB 21; Length 775;
                                                                                                                                                                                                                                                                                                                                                        166; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 -----LATAPR----IDDEIPPPLPVRTPESFIVVE 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNYSL----
                                                                                                                                                                                                                                                                                                     Query Match
31.2%; Score 1127.5; DB
Best Local Similarity 36.6%; Pred. No. 4.2e-87
Matches 280; Conservative 109; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY67251 standard; protein; 775 AA.
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                                                                                                                                                                                                                        775 AA;
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Novel therapeutic agents for treating diseases which are related to cell proliferation, migration, inflammation and angiogenesis especially
                                     Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion; cell migration; division; cytostatic; antiinflammatory; angiogenesis; cancer; enzyme substrate identification; mutein; mouse.
                                                                                                             /note= "Wild-type Cys has been replaced with Ser"
                       PTP-PEST (C231S) amino acid sequence.
                                                                                                                                                                                                                      Angers-Lousteau A,
                                                                                        Location/Qualifiers
231
                                                                                                                                                                                                                                                                                  Claim 17; Page -; 91pp; English.
                                                                                                                                                             99WO-CA00461
                                                                                                                                                                                    98US-0111993
                                                                                                                                                                            98CA-2238654
       (first entry)
                                                                                                                                                                                                                   Cote J,
                                                                                                                                                                                                     (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                    WPI; 2000-097104/08
                                                                                                     Misc-difference
                       Mutant mouse
                                                                                                                                                                                                                     remblay ML,
                                                                                                                             WO9961467-A2
                                                                                                                                                            21-MAY-1999;
       05-APR-2000
                                                                                                                                                                            21-MAY-1998;
                                                                                                                                                                                     11-DEC-1998;
                                                                                                                                             12-DEC-1999
                                                                     Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                     cancer
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Charest A;

This is the amino acid sequence of mouse (C231S) mutant protein tyrosine phosphatase (PTP) PEST. The wild-type cysteine residue at position 231 is replaced with a serine residue. PTP-PEST is a soluble PTP that is ubiquitously expressed throughout embryonic development and in murine adult tissues. The N-terminal portion of the enzyme encodes for the catalytic domain, while the C-terminal portion is composed of 5 proline. In the Omeans, and a binding site for the adaptor protein Shc. The pro 2 domain is required for paxillin binding, and the synthesis of mutant PTP-PEST have shown that proline 362 is important for paxillin binding artifutly. The invention relates to a compound that is capable of a critisty. The invention relates to a compound that is capable of are involved in cell migration, adhesion or division. The compound can be derived from minimal sequences found in binding sites of PTP-PEST. The invention also relates to a method for finding a genuine substrate for an enzyme in a cell that normally expresses the wild type form of the enzyme. A mutant version of PTP-PEST (represented by this sequence) is used in this method. The compounds have cytostatic and antiinflammatory activity. The compounds are used for making medicaments for treating a disease related with cell proliferation, migration, inflammation and angiogenesis, especially cancer. The novel method is used for identifying a genuine substrate for an enzyme. Note: The present sequence is not shown in the specification but it has been derived from the PTP-PEST sequence (see AAY67250) shown in figure

Sequence

28; DB 21; Length 775; 167; Indels 30.9%; Score 1117.5; D 36.5%; Pred. No. 3e-86; iive 109; Mismatches 1 Conservative Similarity Local Simi Query Match Best Loca Matches

1 MDOREILOKFLDEAOSKKIT----KEEFANEFLKLKROSTKYKADKTYPTTVAENAKNIK 56

ð q

WO200055173-A1 21-SEP-2000.

Breast and ovarian cancer associated antigen protein sequence SEQ ID 606. 603 IKE------SSSFDFRTS-----EISAKEELVLHPAKSSTSF 379 DFLELNYSFDKNADTTMKW-------QTKAFPIVGEPLQK-HQSLDLGSLLF 423 403 ---dlnrsydksad---qwgksesaiehidkklernlsfeikkvplqegpksfdgntlln 456 547 -----trnktsistasat-vspassaesachrrv 645 Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rhemmatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease. KNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQGPLSTTLLDFWRM 116 IWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAEKRKSDYIIRTLKV 176 |||||:|:|||||| |:|||:||||||| || : | || :||| |: ::|| |||| : iweynvviivmacrefemgrkkcerywplygedpitfapfkisceneqartdyfirtlll 180 KFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPICIHCSAGCGRTGV 236 ICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMD 296 V-----IRDKHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAKMMNQQRTKME 348 EGCSNSKPVNAAGRYFNSKVPITRTKSTPFEL-----IQQRETKEV----- 464 rg--haikiksa----sssvvdrt-skpqelsagalkvddvsqnscadcsaahshraae 508 HQIRNASN-----YKHHDSSALGVYSYIPLVENP-----YFSSWPPSGTS 561 qtlktvsstpnstaeeeahdltehhnss-----pllkaplsftnplhsddwhsdggs 548 SKMSLDLPEKODGTVFPSSLLPTSSTSLFSYYNSHSSLSLNSPTNISSLLNQESAV--------LATAPR-----IDDEIPPPLPVRTPESFIVVE 630 DSKENFSYLESQPHDSCFVEMQAQKVMHVSSAELNYSL-----AAB58898 standard; Protein; 331 AA. 27-MAR-2001 (first entry) s-----dgav----AAB58898; RESULT 13 457 165 61 121 177 181 297 349 380 613 604 117 AAB58898 q ŏ q g ò g δ g g ŏ qq ò g óγ a δ 셤 δλ g à ŏ δ

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08:33:57 2002
Tue May
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between a protein tyrosine phosphatase (PFP) and a tyrosine phosphatase phosphorylated polypeptide using fluorescence energy signals. The methods are useful for performing screening assay to identify agents that alter PTP binding to and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence is that of a catalytic domain of a PTP for comparison with human PTPIB (AAG78262).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying agents which alter the interaction
  PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide; dephosphorylation; phosphotyrosine; human; PTPlB; mouse; fruit fly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 YPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 GPLSTTLLDFWRMIWEYSVLIIVWACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 KRKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSIDPILELIWDVRCYQEDDSVPI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 CIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 YNAVLELFKRQMDVIRDKHSGTESQAKHCIPEKNHTLQADSYSPNLPKSTTKAAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 hraiaqlfekqlq----lyaidytwnl---lkagkipeef
                                                                                                                                                                                                                                                                                                                                                                                                                                Screening assays to identify agents that alter protein tyrosine phosphatase (PTP) binding to, and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%; Score 933; DB 22;
54.2%; Pred. No. 3.9e-71;
ive 47; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 ----MMNQQRTKMEIKESSSFDFRTSEISAKEELVL 370
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                                                                                                                                                                                                                13-FEB-2001; 2001WO-US05180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB59383 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                Cool DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                                                                                                   (CEPT-) CEPTYR INC
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                                                                                                                             WO200161031-A2
                                                                                     Homo sapiens.
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phosphatase
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                                                                                                                                                                     23-AUG-2001
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                                            yeast.
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                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the sequences AAF22032 - AAF22040 and AAB59129 which are used in the sequences and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic, neuroprotective; antiviral; antivinal; and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis, articularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, correction and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, arthritis and ulcerative colitis; cardiovascular disorders such as mycardial ischaemias; wound healing; neurological diseases such as mycardial anoxia and epilepsy; and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                 New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 HDSCFVEMQAQKVMHVSSAELNYSLPYDSKHQIRNASNVKHHDSSALGVYSYIPLVENPY 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 FSSWPPSGTSSKMSLDLPEKQDGTVFPSSLLPTSSTSLFSYYNSHSSLSLNSPTNISSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 NQESAVLATAPRIDDEIPPPLPVRTPESFIVVEEAGEFSPNVPKSLSSAVKVKIGTSLEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1058; DB 21;
Pred. No. 8.9e-82;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 1045-1047; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     658 GGTSEPKKFDDSVILRPSKSVKLRSPKS 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                  SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.3%;
ilarity 99.0%;
Conservative
             08-MAR-2000; 2000WO-US05881.
                                                     99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-2001 (first entry)
                                                                                                (HUMA-) HUMAN GENOME
                                                                                                                                          Ruben SM;
                                                                                                                                                                                     WPI; 2000-611515/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 AA;
                                                                                                                                                                                                              N-PSDB; AAF21801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PTP-PEST
                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206;
                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG78281;
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RESULT 1

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 GPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWAEPGEMQLEFGPFSVSCEAE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 YPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSYINANFIKGVYGPKAYIATQ 103
                                                                                                                                                                                                                                                                                                                  New substrate trapping mutant protein tyrosine phosphatases (PTP) in which the wild type PTP catalytic domain invariant aspartate is replaced with an unphosphorylated amino acid, useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 253;
                                    Protein tyrosine phosphatase; human; mouse; fruit fly; PTP; substrate trapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.5%; Score 921.5; DB 2:
65.4%; Pred. No. 2.7e-70;
tive 41; Mismatches 44
             Human protein tyrosine phosphatase #14.
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 109pp; English.
                                                                                                                                                                                                                                    (COLD-) COLD SPRING HARBOR LAB
                                                                                                                                                                                            99US-0137319.
99US-0334575.
                                                                                                                                                                24-MAY-2000; 2000WO-US14211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 65.49
Matches 166; Conservative
                                                                                                                                                                                                                                                                                          WPI; 2001-080598/09
                                                                                                                                                                                                                                                                Zhang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 AA;
                                                                                                         WO200075339-A1
                                                                               Homo sapiens.
                                                                                                                                                                                            03-JUN-1999;
16-JUN-1999;
                                                                                                                                     14-DEC-2000
                                                                                                                                                                                                                                                                Tonks NK,
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